

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 5, 2006, 15:52:10 ; Search time 22 Seconds

(without alignments)
529.192 Million cell updates/sec

Title: US-09-560-494E-24

Perfect score: 642
Sequence: 1 MSQPRVSPDLRTWMLGRTVE.....IMVSHFVPVFLPAKPTTTP 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	637	99.2	235	1 RWHUT8	T-cell surface gly
2	599	93.3	198	2 S35656	T-cell surface gly
3	366.5	57.1	239	2 I46082	CD8 alpha-chain -
4	347.5	54.1	242	2 S25663	T-cell surface gly
5	248	38.6	236	2 A24637	T-cell surface gly
6	239	37.2	247	1 RWMST2	T-cell surface gly
7	238	37.1	220	2 I55963	Lyt-2.1 lymphocyte
8	238	37.1	247	2 A34954	T-cell surface gly
9	227.5	35.4	246	2 A29523	T-cell surface gly
10	155	24.1	235	2 I50610	T-cell surface gly
11	130.5	20.3	230	2 S49449	T-cell surface gly
12	122.5	19.1	213	2 A21177	Ig lambda chain -
13	121.5	18.9	105	2 S38495	Ig lambda chain -
14	120.5	18.8	107	2 PL0080	Ig kappa chain V r
15	119.5	18.6	107	2 S38495	Ig kappa chain V r
16	119	18.5	99	2 S36058	Ig lambda chain -
17	117.5	18.3	113	1 L1CHV	Ig lambda chain pr
18	117.5	18.3	125	2 A31493	Ig light chain pre
19	116.5	18.1	233	2 S25744	Ig lambda chain -
20	116	18.1	231	2 S25753	Ig lambda chain -
21	114	17.8	151	2 S24084	T-cell receptor be
22	113	17.6	146	2 S02083	Ig lambda chain V r
23	111.5	17.4	108	1 KVM506	Ig kappa chain V r
24	111	17.3	112	2 S46395	Ig lambda chain V
25	111	17.3	112	2 S09970	Ig kappa chain V-J
26	111	17.3	219	2 S38865	Ig kappa chain - m
27	110.5	17.2	107	2 S12954	Ig kappa chain V r
28	110.5	17.2	114	2 S40375	Ig kappa chain - h
29	110.5	17.2	235	2 S25758	Ig lambda chain -

30	110	17.1	99	2 S36056	Ig lambda chain -
31	110	17.1	112	2 S58207	Ig light chain V r
32	110	17.1	132	2 S26882	Ig kappa chain V r
33	110	17.1	135	2 S40342	Ig kappa chain - h
34	110	17.1	136	2 S40357	Ig kappa chain V-J
35	110	17.1	231	2 S25751	Ig lambda chain -
36	109.5	17.1	97	2 I51216	Ig light chain var
37	109.5	17.1	98	2 PH1069	Ig light chain V r
38	109.5	17.1	106	2 B47329	Ig kappa chain V r
39	109.5	17.1	111	2 S36281	Ig lambda chain V
40	109.5	17.1	112	2 S58206	Ig light chain V r
41	109.5	17.1	113	2 KVM526	Ig kappa chain V r
42	109.5	17.1	128	2 S31488	Ig kappa chain pre
43	109.5	17.1	132	2 PH0106	anti-digoxin trans
44	109.5	17.1	233	2 S25741	Ig lambda chain -
45	109	17.0	110	1 L2H058	Ig lambda chain V-

ALIGNMENTS

RESULT 1
RWHUT8
T-cell surface glycoprotein CD8 alpha chain precursor - human
N:Alternate names: Leu-2/T8 T lymphocyte differentiation antigen; T-cell surface antigen
N:Contains: T-cell surface glycoprotein CD8 alpha chain secreted splice form; T-cell su
C:Species: Homo sapiens (man)
C:Date: 28-May-1986 #sequence revision 28-May-1986 #text change 09-Jul-2004
C:Accession: A30604; A45888; A01999; A22824; A50096; A31458; B31458; J0105
R:Normant, A.M.; Lombey, N.; Lacy, E.; Littman, D.R.
J. Immunol. 142, 3312-3319, 1989
A:Title: Alternately spliced mRNA encodes a secreted form of human CD8-alpha. Charact
A:Reference number: A30604; MUID:89215302; PMID:2496167
A:Accession: A30604
A:Molecule type: DNA
A:Residues: 1-235 <NOR>
A:Cross-references: UNIPARC:UPI00001273B4; GB:M27161; NID:g187844; PIDN:AAA5674.1; PID
R:Nakayama, K.; Tokito, S.; Okumura, K.; Nakauchi, H.
Immunogenetics 30, 393-397, 1989
A:Title: Structure and expression of the gene encoding CD8-alpha chain (Leu-2/T8).
A:Reference number: A45888; MUID:90035142; PMID:2509342
A:Accession: A45888
A:Molecule type: DNA
A:Residues: 1-235 <NAK>
A:Cross-references: UNIPARC:UPI00001273B4; GB:M27161; NID:g187844; PIDN:AAA5674.1; PID
R:Littman, D.R.; Thomas, Y.; Maddon, P.J.; Chess, L.; Axel, R.
Cell 40, 237-246, 1985
A:Title: The isolation and sequence of the gene encoding T8: a molecule defining functi
A:Reference number: A01999; MUID:85099337; PMID:3871356
A:Accession: A01999
A:Molecule type: mRNA
A:Residues: 1-235 <LIT>
A:Cross-references: UNIPARC:UPI00001273B4; GB:M12828; NID:g179145; PIDN:AA04637.1; PID
R:Experimental source: clones pT8.B and pT8.F1
A:Substrate: V.P.; Sizer, K.C.; Vollmer, A.C.; Hunkapiller, T.; Parnes, J.R.
Cell 40, 551-597, 1985
A:Title: The T cell differentiation antigen Leu-2/T8 is homologous to immunoglobulin an
A:Reference number: A22824; MUID:85124610; PMID:3918796
A:Accession: A22824
A:Molecule type: mRNA
A:Residues: 1-235 <SUK>
A:Cross-references: UNIPARC:UPI00001273B4; GB:M12824; NID:g339426; PIDN:AAA61133.1; PID
R:Parnes, J.R.; Sizer, K.C.; Sukhatme, V.P.; Hunkapiller, T.
Behring Inst. Mitt. 77, 48-55, 1985
A:Title: Structure of Leu-2/T8 as deduced from the sequence of a cDNA clone.
A:Reference number: A90096; MUID:86103103; PMID:3336473
A:Accession: A90096
A:Molecule type: mRNA
A:Residues: 1-235 <PAR>
A:Cross-references: UNIPARC:UPI00001273B4
R:Giblin, P.; Ledbetter, J.A.; Kavathas, P.
Proc. Natl. Acad. Sci. U.S.A. 86, 998-1002, 1989

A>Title: A secreted form of the human lymphocyte cell surface molecule CD8 arises from A
 A/Accession: A31458; MID:89180905; PMID:2556961
 A/Status: nucleic acid sequence not shown; not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 168-235 <GIB>
 A/Cross-references: UNIPARC:UPI0000173727
 A/Note: this mRNA fragment represents the transmembrane form
 A/Accession: B31458
 A/Status: nucleic acid sequence not shown; not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 168-171, 'G', 210-235 <G12>
 A/Cross-references: UNIPARC:UPI0000173728
 A/Note: this mRNA fragment represents the secreted form
 A/Note: the cited Genbank accession number, J04165, is not in release
 R/snow, P.M.; Thorbert, C.
 U. Biol. Chem. 258, 14675-14681, 1983
 A/Reference number: A92407; MID:84061928; PMID:6605969
 A/Contents: annotation
 C/Comment: This protein was shown in reference A92407 to be in a multimeric complex of C
 C/Genetics: Alternative splicing leads to the production of a secreted form lacking the C
 A/Accession: GDB:CD8A
 A/Cross-references: GDB:120581; OMIM:186910
 A/Map position: 2p12-2p12
 A/Intons: 17/1; 135/1; 172/1; 209/1; 219/2
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: alternative splicing; extracellular protein; glycoprotein; heterotetramer; I
 F/1-21/Domain: signal sequence #status predicted <SIG>
 F/22-235/Product: T-cell surface glycoprotein CD8 alpha chain transmembrane splice form
 F/22-171, 209-235/Product: T-cell surface glycoprotein CD8 alpha chain secreted splice fo
 F/36-117/Domain: immunoglobulin homology <IMM>
 F/118-182/Domain: hinge <HNG>
 F/183-205/Domain: transmembrane #status predicted <TMB>
 F/206-235/Domain: intracellular #status predicted <INT>
 F/43-115/Dismulfide bonds: #status predicted
 F/49/Binding site: carbohydrate (asn) (covalent) #status predicted
 F/181/Dismulfide bonds: interchain #status predicted

Query Match 99.2%; Score 637; DB 1; Length 235;
 Best Local Similarity 100.0%; Pred. No. 2.6e-56;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SGRVSPDLRTNMLGTEVLEKCOVLTLSNPTSGCSWLFQPRGAASPTFLYLTSQNKPKAA 61
 DB 22 SGRVSPDLRTNMLGTEVLEKCOVLTLSNPTSGCSWLFQPRGAASPTFLYLTSQNKPKAA 81

QY 62 EGLDTRFGSGKRLGDTFVLTLSDFRRENGYFCSALNSIMYFSHFVFPVFLPAKPTTP 121
 DB 82 EGLDTRFGSGKRLGDTFVLTLSDFRRENGYFCSALNSIMYFSHFVFPVFLPAKPTTP 141

RESULT 2

S25656
 T-cell surface glycoprotein CD8 alpha chain precursor - orangutan
 C/Species: Pongo pygmaeus (orangutan)
 C/Date: 26-Feb-1998 #sequence_rev1510n 26-Feb-1998 #text_change 09-Jul-2004
 C/Accession: S25656
 R/Lawlor, D.A.; Parham, P.
 Immunogenetics 36, 121-125, 1992
 A/Title: Structure of CD8 alpha and beta chains of the orangutan: novel patterns of mRNA
 A/Reference number: S25656; MID:92307742; PMID:1612644
 A/Accession: S25656
 A/Molecule type: mRNA
 A/Residues: 1198 <LAW>
 A/Cross-references: UNIPROT:P30433; UNIPARC:UPI00001273B5; EMBL:X60223; NID:G38144; PIDN
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: alternative splicing; extracellular protein; glycoprotein; heterotetramer; I
 F/1-21/Domain: signal sequence #status predicted <SIG>
 F/22-198/Product: T-cell surface glycoprotein CD8 alpha chain transmembrane splice fo
 F/36-117/Domain: immunoglobulin homology <IMM>
 F/146-168/Domain: transmembrane #status predicted <TMB>
 F/169-198/Domain: intracellular #status predicted <INT>

F/43-115/Dismulfide bonds: #status predicted
 F/49/Binding site: carbohydrate (asn) (covalent) #status predicted
 F/144/Dismulfide bonds: interchain #status predicted

Query Match 93.3%; Score 599; DB 2; Length 198;
 Best Local Similarity 100.0%; Pred. No. 1.4e-52;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SGRVSPDLRTNMLGTEVLEKCOVLTLSNPTSGCSWLFQPRGAASPTFLYLTSQNKPKAA 61
 DB 22 SGRVSPDLRTNMLGTEVLEKCOVLTLSNPTSGCSWLFQPRGAASPTFLYLTSQNKPKAA 81

QY 62 EGLDTRFGSGKRLGDTFVLTLSDFRRENGYFCSALNSIMYFSHFVFPVFLPAKPTTP 114
 DB 82 EGLDTRFGSGKRLGDTFVLTLSDFRRENGYFCSALNSIMYFSHFVFPVFLPAKPTTP 134

RESULT 3

146082
 CD8 alpha-chain - cat
 C/Species: Felis silvestris catus (domestic cat)
 C/Date: 16-Aug-1996 #sequence_rev1510n 16-Aug-1996 #text_change 09-Jul-2004
 C/Accession: I46082
 R/Pecoraro, M.; Kawaguchi, Y.; Miyazawa, T.; Norimine, J.; Maeda, K.; Toyosaki, T.; Tohy
 Immunology 81, 127-131, 1994
 A/Title: Isolation, sequence and expression of a cDNA encoding the alpha-chain of the f
 A/Reference number: I46082; MID:9418799; PMID:8132208
 A/Accession: I46082
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-239 <EBC>
 A/Cross-references: UNIPROT:P41688; UNIPARC:UPI00001273B3; GB:D16536; NID:G485385; PIDN
 C/Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 57.1%; Score 366.5; DB 2; Length 239;
 Best Local Similarity 58.7%; Pred. No. 3e-29;
 Matches 71; Conservative 19; Mismatches 30; Indels 1; Gaps 1;

QY 2 SGRVSPDLRTNMLGTEVLEKCOVLTLSNPTSGCSWLFQPRGAASPTFLYLTSQNKPKAA 61
 DB 25 SGRVSPDLRTNMLGTEVLEKCOVLTLSNPTSGCSWLFQPRGAASPTFLYLTSQNKPKAA 84

QY 62 EGLDTRFGSGKRLGDTFVLTLSDFRRENGYFCSALNSIMYFSHFVFPVFLPAKPTTP 120
 DB 85 EGLDTRFGSGKRLGDTFVLTLSDFRRENGYFCSALNSIMYFSHFVFPVFLPAKPTTP 144

QY 121 P 121
 DB 145 P 145

RESULT 4

S25663
 T-cell surface glycoprotein CD8 alpha chain - bovine
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 13-Jan-1995 #sequence_rev1510n 13-Jan-1995 #text_change 09-Jul-2004
 C/Accession: S25663
 R/Lawlor, P.; Buccil, C.; Fornaro, M.; Rattazzi, M.C.; Nakachi, H.; Herzenberg, L.A.; Al
 Immunology 76, 95-102, 1992
 A/Title: Molecular cloning, reconstruction and expression of the gene encoding the alph
 A/Reference number: S25663; MID:92332098; PMID:1628904
 A/Accession: S25663
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1242 <LAW>
 A/Cross-references: UNIPROT:P31783; UNIPARC:UPI00001273B1; EMBL:X59416; NID:G190; PIDN
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: glycoprotein; transmembrane protein

Query Match 54.1%; Score 347.5; DB 2; Length 242;
 Best Local Similarity 57.1%; Pred. No. 2.4e-27;
 Matches 60; Conservative 17; Mismatches 33; Indels 1; Gaps 1;

RESULT 8

A34954
T-cell surface glycoprotein Lyr-2 precursor (strain C.AKR) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 07-Sep-1990 #sequence_revision 03-Jun-1993 #text_change 21-Jan-2000
C/Accession: A34954
R/Youn, H.J.; Harries, J.V.; Gottlieb, P.D.
Immunogenetics 28, 345-352, 1988
A/Title: Nucleotide sequence analysis of the C.AKR Lyr-2(a) gene: structural polymorphism
A/Reference number: A34954; MUID:89006895; PMID:3267233
A/Accession: A34954
A/Molecule type: DNA
A/Residues: 1-247 <YOU>
A/Cross-references: UNIPARC:UPI000016CEPF; GB:M22064; NID:G199569; PIDN:AAA39665.1; PID:
A/Note: the authors translated the codon CCR for residue 208 as Leu
C/Genetics:
A/Intons: 149/1; 184/1; 221/1; 231/2
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: glycoprotein; transmembrane protein
F/1-27/Domain: signal sequence #status predicted <SIG>
F/28-247/Product: T-cell surface glycoprotein Lyr-2 #status predicted <MAT>
F/46-131/Domain: immunoglobulin homology <IMM>

Query Match 37.1%; Score 238; DB 2; Length 247;

Best Local Similarity 44.7%; Pred. No. 2.2e-16;

Matches 55; Conservative 20; Mismatches 42; Indels 6; Gaps 5;

QY 3 QFVSPIDRTWNLGETVELKCOVLISNPTSGCSWLFQPRGA--AASPTFLYL--SOKPK 59

DB 33 ELRIFPKMDAELGQKVDLVCEV--LGSVSGCSWLFQNSSSKLPQPTFVYMASSHNKIT 91

QY 60 AAGLDLQDQ--FSGKR--LGDPTFVLTLSDFRRENEGYYFCALSINSIMVFSHFVPLPAKP 117

DB 92 WDEKLNSKLPFAVRDPTNNKIVLTINKFSKENEGYFCVINSVMTFSSVVPVLQKVNST 151

QY 118 TTT 120

DB 152 TTT 154

RESULT 9

A29523
T-cell surface glycoprotein Lyr-2 precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C/Accession: A29523
R/Nakauchi, H.; Tagawa, M.; Nolan, G.P.; Herzenberg, L.A.
Nucleic Acids Res. 15, 4337-4347, 1987
A/Title: Isolation and characterization of the gene for the murine T cell differentiatid
A/Reference number: A29523; MUID:87231009; PMID:3495785
A/Accession: A29523
A/Molecule type: DNA
A/Residues: 1-246 <NKA>
A/Cross-references: UNIPROT:P01731; UNIPARC:UPI000016CEC2; GB:Y00157; NID:G52967; PIDN:C
C/Genetics:
A/Intons: 148/1; 183/1; 220/1; 230/2
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: glycoprotein; transmembrane protein
F/46-130/Domain: immunoglobulin homology <IMM>

Query Match 35.4%; Score 227.5; DB 2; Length 246;

Best Local Similarity 44.3%; Pred. No. 2.4e-15;

Matches 54; Conservative 19; Mismatches 44; Indels 5; Gaps 5;

QY 3 QFVSPIDRTWNLGETVELKCOVLISNPTSGCSWLFQPRGA--AASPTFL--LYLSOKPKA 60

DB 33 ELRIFPKMDAELGQKVDLVCEV--LGSVSGCSWLFQNSSSKLPQPTFVYMASSHNKITW 91

QY 61 AAGLDLQDQ--FSGKR--LGDPTFVLTLSDFRRENEGYYFCALSINSIMVFSHFVPLPAKP 118

DB 92 DEKLNSKLPFAVRDPTNNKIVLTINKFSKENEGYFCVINSVMTFSSVVPVLQKVNST 151

QY 119 TT 120

DB 152 TT 153

RESULT 10

I50610
T-cell surface glycoprotein CD8 alpha chain - chicken
C/Species: Gallus gallus (chicken)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C/Accession: I50610; S33350
R/Tregaskes, C.A.; Kong, F.K.; Parmitiotis, E.; Chen, C.L.; Ratcliffe, M.J.; Davison, J.; Immunol. 154, 4485-4494, 1995
A/Title: Identification and analysis of the expression of CD8 alpha beta and CD8 alpha
lymphocytes.
A/Reference number: I50609; MUID:95238946; PMID:7722305
A/Accession: I50610
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-235 <TRE>
A/Cross-references: UNIPROT:Q90770; UNIPARC:UPI00000FBABF; EMBL:Z22726; NID:G488149; PI
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: glycoprotein

Query Match 24.1%; Score 155; DB 2; Length 235;

Best Local Similarity 30.7%; Pred. No. 4e-08;

Matches 35; Conservative 24; Mismatches 37; Indels 18; Gaps 4;

QY 16 GETVELKCOVLISNPTSGCSWLFQPRGAASPTFLYL-----QNKPKAAGLDIQ 67

DB 42 GQRLTECRPF--NSDNGVSWIRQDKLH--FIVYISPLSTPTTPQNERISSQ----- 92

QY 68 RFGSKRLGDTFVLTLSDFRRENEGYYFCALSINSIMVFSHFVPLPAKPTTP 121

DB 93 -FSGSKSGSFRVAVNFKRQDQTYFCIANIQMVIYFSGCGAFAPATTAA 145

RESULT 11

S49449
Ig lambda chain - duck
C/Species: Anas platyrhynchos (domestic duck)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C/Accession: S49449
R/Magor, K.B.; Higgins, D.A.; Middleton, D.L.; Watt, G.W.
submitted to the EMBL Data Library, October 1994
A/Description: cDNA sequence and organization of the immunoglobulin light chain gene of
A/Reference number: S49449
A/Accession: S49449
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-230 <MAG>
A/Cross-references: UNIPARC:UPI00001161F6; EMBL:X82069; NID:G558548; PIDN:CAA57568.1; P
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/34-106/Domain: immunoglobulin homology <IMM>

Query Match 20.3%; Score 130.5; DB 2; Length 230;

Best Local Similarity 29.5%; Pred. No. 1.1e-05;

Matches 31; Conservative 21; Mismatches 38; Indels 15; Gaps 4;

QY 8 PLDRTNWLGTEVELKCOVLISNPTSGCSWLFQPRGAASPTFLYLISYSONKPKAAGLDIQ 67

DB 26 PAKSVVPGDTVOITC---SGSSSDYGV--FOOKTPGSAVTVIYONNKRPSGI---PS 76

QY 68 RFGSKRLGDTFVLTLSDFRRENEGYYFCALSINSIMVFSHFVPL 112

DB 77 RFGSKSGSFRVAVNFKRQDQTYFCIANIQMVIYFSGCGAFAPATTAA 115

RESULT 12

A21177
I light chain precursor V-J region - chicken (fragment)
C/Species: Gallus gallus (chicken)

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OM protein - protein search, using sw model

Run on: April 5, 2006, 15:54:26 ; Search time 25 Seconds
(without alignments)
150.969 Million cell updates/sec

Title: US-09-560-494E-24

Perfect score: 642
Sequence: 1 MSQFRVSPDLRTWNLGETVR.....IMYPSHFVPLPAKPTTTP 121

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 184161

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Published Applications_AA_New*

1: /SIDS5/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /SIDS5/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /SIDS5/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /SIDS5/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
5: /SIDS5/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
6: /SIDS5/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
7: /SIDS5/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /SIDS5/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	131	20.4	110	US-11-049-536-652	Sequence 652, App
2	131	20.4	110	US-11-199-739-652	Sequence 652, App
3	123.5	19.2	252	US-11-054-515-1954	Sequence 1854, App
4	123.5	19.2	252	US-11-266-444-1954	Sequence 1854, App
5	119.5	18.6	98	US-11-084-554-202	Sequence 202, App
6	119.5	18.6	98	US-11-136-250-202	Sequence 202, App
7	119	18.5	99	US-11-084-554-206	Sequence 206, App
8	119	18.5	99	US-11-136-250-206	Sequence 206, App
9	119	18.5	109	US-10-952-535A-4	Sequence 4, App1
10	119	18.5	109	US-10-771-257-64	Sequence 64, App1
11	119	18.5	109	US-11-127-677-62	Sequence 62, App1
12	118.5	18.5	239	US-10-952-535A-6	Sequence 6, App1
13	118.5	18.5	112	US-10-982-440-12	Sequence 12, App1
14	118.5	18.5	250	US-10-512-184-27	Sequence 27, App1
15	118.5	18.5	250	US-11-054-515-1833	Sequence 1833, App
16	118.5	18.5	251	US-11-266-444-1833	Sequence 1833, App
17	118.5	18.5	252	US-11-054-515-1475	Sequence 1475, App
18	118.5	18.5	252	US-11-266-444-1475	Sequence 1475, App
19	118	18.4	110	US-11-049-536-500	Sequence 500, App
20	118	18.4	110	US-11-199-739-500	Sequence 500, App
21	117.5	18.3	252	US-11-054-515-1376	Sequence 1376, App
22	117.5	18.3	252	US-11-266-444-1376	Sequence 1376, App
23	116.5	18.1	108	US-11-127-677-77	Sequence 77, App1
24	116.5	18.1	111	US-11-049-536-692	Sequence 692, App
25	116.5	18.1	111	US-11-199-739-692	Sequence 692, App

26	116.5	18.1	142	7	US-11-049-536-74	Sequence 74, App1
27	116.5	18.1	142	7	US-11-199-739-74	Sequence 74, App1
28	115.5	18.0	246	7	US-11-054-515-1980	Sequence 1980, App
29	115.5	18.0	246	7	US-11-266-444-1980	Sequence 1980, App
30	115.5	18.0	248	7	US-11-054-515-921	Sequence 921, App
31	115.5	18.0	248	7	US-11-054-515-1251	Sequence 1251, App
32	115.5	18.0	248	7	US-11-266-444-921	Sequence 921, App
33	115.5	18.0	248	7	US-11-266-444-1251	Sequence 1251, App
34	115.5	18.0	256	7	US-11-054-515-1026	Sequence 1026, App
35	115.5	18.0	256	7	US-11-266-444-1026	Sequence 1026, App
36	115.5	18.0	257	7	US-11-054-515-1283	Sequence 1283, App
37	115.5	18.0	257	7	US-11-266-444-1283	Sequence 1283, App
38	115	17.9	327	6	US-10-512-184-62	Sequence 62, App1
39	115	17.9	327	6	US-10-512-184-64	Sequence 62, App1
40	115	17.9	327	6	US-10-512-184-63	Sequence 64, App1
41	115	17.9	328	6	US-10-512-184-65	Sequence 64, App1
42	115	17.9	576	6	US-10-512-184-65	Sequence 65, App1
43	115	17.9	625	6	US-10-512-184-67	Sequence 47, App1
44	114.5	17.8	122	6	US-10-993-543-174	Sequence 174, App
45	114.5	17.8	245	7	US-11-054-515-1523	Sequence 1523, App

ALIGNMENTS

```
RESULT 1
US-11-049-536-652
Sequence 652, Application US/11049536
GENERAL INFORMATION:
APPLICANT: Wood, Clive R.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Pieters, Henk
APPLICANT: Hoeft, Rene
APPLICANT: Hulton, Simon E.
TITLE OF INVENTION: TIR COMPLEX BINDING PROTEINS
FILE REFERENCE: 10280-128001
CURRENT APPLICATION NUMBER: US/11/049,536
CURRENT FILING DATE: 2005-02-02
PRIOR APPLICATION NUMBER: US 10/916,840
PRIOR FILING DATE: 2004-08-12
PRIOR APPLICATION NUMBER: US 60/494,713
PRIOR FILING DATE: 2003-08-12
NUMBER OF SEQ ID NOS: 721
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 652
LENGTH: 110
TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
FEATURE:
OTHER INFORMATION: Antibody
US-11-049-536-652

Query Match          20.4%; Score 131; DB 7; Length 110;
Best Local Similarity 36.3%; Pred. No. 4.7e-07;
Matches 33; Conservative 14; Mismatches 36; Indels 8; Gaps 3;

QY 16 GETVELKQVLLSNPTS--GCSWLFQPRGAASPTFLYLISONKPKAAGLDIQFSGKR 73
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 15 GQSVTISCTGTSDDVCSYNNVSWYRQBPGR--PKVIYDINNRPQGV---PDRFSGSR 68
QY 74 LGDTFVLTLSDFRRENGGYFCGALSINSIMY 104
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 69 SGGTAVTITISGLQVEDADYTCSSFTSSSTY 99

RESULT 2
US-11-199-739-652
Sequence 652, Application US/11199739
GENERAL INFORMATION:
APPLICANT: Wood, Clive R.
APPLICANT: Dransfield, Daniel T.
```

```

; APPLICANT: Pieters, Henk
; APPLICANT: Hoeft, Rene
; APPLICANT: Hufton, Simon E.
; TITLE OF INVENTION: TIE COMPLEX BINDING PROTEINS
; FILE REFERENCE: 10280-135001
; CURRENT APPLICATION NUMBER: US/11/199,739
; PRIOR FILING DATE: 2005-08-09
; PRIOR APPLICATION NUMBER: US 11/049,536
; PRIOR FILING DATE: 2005-02-02
; PRIOR APPLICATION NUMBER: US 10/916,840
; PRIOR FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: US 60/494,713
; PRIOR FILING DATE: 2003-08-12
; NUMBER OF SEQ ID NOS: 726
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 652
; LENGTH: 110
; TYPE: PRT
; ORGANISM: ARTIFICIAL
; FEATURE:
; OTHER INFORMATION: Antibody
US-11-199-739-652

Query Match          20.4%; Score 131; DB 7; Length 110;
Best Local Similarity 36.3%; Pred. No. 4,7e-07;
Matches 33; Conservative 14; Mismatches 36; Indels 8; Gaps 3;

QY 16 GENEVLKQVLLSNPNS--GCSWLFQPRGAASPTFLVLSQNKPKRAEGLDTPRSGKR 73
DB 15 GQSVTISCTGTSSDVGSYNRWSYRQPGTA--PKVLIYINRPGSV----PDRSGSR 68
QY 74 LGDTFVLTLSDFRRENGEYFCSALSNISY 104
DB 69 SGDTAVLTISGLQVEDEADYCCSFTSSSTY 99

RESULT 3
US-11-054-515-1954
; Sequence 1954, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1954
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1954
```

```

Query Match          19.2%; Score 123.5; DB 7; Length 252;
Best Local Similarity 31.2%; Pred. No. 7,4e-06;
Matches 30; Conservative 17; Mismatches 42; Indels 7; Gaps 3;

QY 8 PLDRTNLGEVELKQVLLSN-PTSGCSWLFQPRGAASPTFLVLSQNKPKRAEGLDT 66
DB 148 PSSASGTLGQRLISICSGSSNSVSWYHQVAGTA--PKLLIYGSDBRPSGV----P 201
QY 67 QRFSGRLDPTFVLTLSDFRRENGEYFCSALSNST 102
DB 202 YRFSGSGKSTLSALSLRSEDEGDIYCATWDSL 237

RESULT 4
US-11-266-444-1954
; Sequence 1954, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; PRIOR FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1954
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-1954

Query Match          19.2%; Score 123.5; DB 7; Length 252;
Best Local Similarity 31.2%; Pred. No. 7,4e-06;
Matches 30; Conservative 17; Mismatches 42; Indels 7; Gaps 3;

QY 8 PLDRTNLGEVELKQVLLSN-PTSGCSWLFQPRGAASPTFLVLSQNKPKRAEGLDT 66
DB 148 PSSASGTLGQRLISICSGSSNSVSWYHQVAGTA--PKLLIYGSDBRPSGV----P 201
QY 67 QRFSGRLDPTFVLTLSDFRRENGEYFCSALSNST 102
DB 202 YRFSGSGKSTLSALSLRSEDEGDIYCATWDSL 237

RESULT 5
US-11-084-554-202
; Sequence 202, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Strid-Al
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Moutier
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
; FILE REFERENCE: ABGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
```



```

? PRIOR FILING DATE: 2004-05-24
? NUMBER OF SEQ ID NOS: 266
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 202
? LENGTH: 98
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-11-084-554-202

```

Query Match	18.6%	Score 119.5	DB 7	Length 98
Best Local Similarity	34.1%	Pred. No. 6.9e-06		
Matches 31, Conservative	17	Mismatches 32	Indels 11	Gaps 4

Dy 15 LGRTVELK---QVLSNPTSGCWMFPGRGAASPTFLLYLSQNKPKAEBGLDTRPSFG 71
Db 14 LRQTATLTCTGNSNIYGN--QGAWLQHOG--HPPKLISYRNRRNPSPGI---SERFSA 65

```
QY      72 KRGLDITVLTLSDFRREHEGIIYPCSA LNSI 102
        |::| :: :||| ::|:
Db      66 SRSGNTASLTITGLQPDEADYYCSAL DSSL 96
```

RESULT 6
US-11-13

```

Sequence 202, Application US/11136250
Publication No. US20060021074A1
GENERAL INFORMATION:
APPLICANT: Kellermann, Sirdi-Ai
APPLICANT: Green, Larry L.
APPLICANT: Koverer, Wouter
TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
FILE REFERENCE: ABGENIX.100A2
CURRENT APPLICATION NUMBER: US/11/136,250
PRIORITY FILING DATE: 2005-05-23
PRIORITY APPLICATION NUMBER: 11/084,554
PRIORITY FILING DATE: 2005-03-17
PRIORITY APPLICATION NUMBER: PCT/US2005/009306
PRIORITY FILING DATE: 2005-03-17
PRIORITY APPLICATION NUMBER: 60/574,661
PRIORITY FILING DATE: 2004-05-24
PRIORITY APPLICATION NUMBER: 60/554,372
PRIORITY FILING DATE: 2004-03-19
NUMBER OF SEQ ID NOS: 266
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 202
LENGTH: 98
TYPE: PR1
ORGANISM: Homo sapiens
US-11-136-250-202

```

Query Match	18.6%	Score 119.5;	DB 7;	Length 98;
Best Local Similarity	34.1%	Pred. No. 6.9e-06;		
Matches 31; Conservative	17;	Mismatches 32;	Indels 11;	Gaps 4;

QY 15 LGRIVELK---QVLINPTGSCSMLEQPRGAASPTFLILYLSQNKPKAEBGLDTPRFSG 711

Db 14 LRQTATLTCTGNSNIVGN--QGAAMTQHQG--HPKLSYRNRRNRPISG----SERFSA 655

```

QY      72 KRIGDTFVLTLSDFRENEGYYFCASALNSI 102
          | | | | | : : : | | | | : :
Db      66 SRSNGTASLTITGLQPEDEADYYCSALDSSL 96

```

RESULT 7
US-11-08.

Sequence: 206, Application US/11084554
Publication No. US20050260679A1
GENERAL INFORMATION:
APPLICANT: Kelleermann, Sird-Ai
APPLICANT: Green, Karen, Larry L.
APPLICANT: Kover, Walter
TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN

```

?
? TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
? FILE REFERENCE: ARGEMIX.100A
? CURRENT APPLICATION NUMBER: US/11/084,554
? PRIOR FILING DATE: 2005-03-17
? PRIOR APPLICATION NUMBER: 60/554,372
? PRIOR FILING DATE: 2004-03-19
? PRIOR APPLICATION NUMBER: 60/574,661
? PRIOR FILING DATE: 2004-05-24
? NUMBER OF SEQ ID NOS: 266
? SOFTWARE: PaatSeq for Windows Version 4.0
? SEQ ID NO 206
? LENGTH: 99
? TYPE: PRT
? ORGANISM: Homo sapiens
US-11-084-554-206

```

Query Match	18.5%	Score 119;	DB 7;	length 99;
Best Local Similarity	34.1%	Pred. No. 7.9e-06;		
Matches	30;	Mismatches	35;	Indels
			8;	Gaps
				3;

Dy 16 GETVELKCOVLLSNPTS--GCSWLPQRGAAASPFTLLYLSONPKAEGIDTQPSGKR 73
Db 15 GGSVTISCTGSSDVGSYNRVSWYQQPQTA--PKMTIYEVSNRPSGV----PDPRSGSK 68

```

QY      74 LGDTFVLTLSDFRRRNEGGYFCASALNS 101
      ||| ||| : ||| : ||| : |||
Db      69 SGNFASLTISGLQABDEADYCYSLYTSS 96

```

RESULT 8
US-11-13

```

# Sequence 206, Application US/11136250
# Publication No. US20060021074A1
# GENERAL INFORMATION:
# APPLICANT: Kellermann, Sirdi-Ai
# APPLICANT: Green, Larry L.
# APPLICANT: Korvet, Wouter
# TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
# TITLE OF INVENTION: ANTIBODIES THROUGH V GENE
# FILE REFERENCE: ABGENIX.10042
# CURRENT APPLICATION NUMBER: US/11/136,250
# PRIOR FILING DATE: 2005-05-23
# PRIOR APPLICATION NUMBER: 11/084,554
# PRIOR FILING DATE: 2005-03-17
# PRIOR APPLICATION NUMBER: PCT/US2005/009306
# PRIOR FILING DATE: 2005-03-17
# PRIOR APPLICATION NUMBER: 60/574,661
# PRIOR FILING DATE: 2004-05-24
# PRIOR APPLICATION NUMBER: 60/554,372
# PRIOR FILING DATE: 2004-03-19
# NUMBER OF SEQ ID NOS: 266
# SOFTWARE: FastSeq for Windows Version 4.0
# SEQ ID NO 206
# LENGTH: 99
# TYPE: PR1
# ORGANISM: Homo sapiens
# OS-11-136-250-206

```

Query Match	18.5%	Score 119;	DB 7;	Length 99;
Similarity		Pred. No. 7.9e-06;		
Best Local	34.1%			
Matches 30;	Conservative 15;	Mismatches 35;	Indels 8;	Gaps 34;

Dy 16 GEIVTELKCOVLLSNPTS--GCSWLPOPRGAALSPTELLIYLSQNKPKAAGLDTORPSGKR 73
|:::| | | | | | | | | | | | | | | |
Db 15 GGSVTISTGTSDVGSGYNRVSWMYQQPPGTA--PKMLIEVNSNRPSGV----PDRFSGSK 68

Dy 74 LGDTFVLTLSDFRNEGYYFCASLNS 101
| : | : | : | : | : | :
Db 69 SGNLASLTISGLQADEADYCSLYTSS 96

RESULT 9
US-10-952-535A-4

```
; Sequence 4, Application US/10952535A
; Publication No. US2005025513A1
; GENERAL INFORMATION:
; APPLICANT: Huxton, James S.
; APPLICANT: Messer, Anne
; APPLICANT: Lecert, Jean-Michel
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITTING POLYPEPTIDE
; TITLE OF INVENTION: ACCUMULATION ASSOCIATED WITH NEUROLOGICAL DISORDERS
; FILE REFERENCE: INR-004CP
; CURRENT APPLICATION NUMBER: US/10/952,535A
; PRIOR FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: 60/146,047
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-952-535A-4
```

```
Query Match          18.5%; Score 119; DB 6; Length 109;
Best Local Similarity 34.1%; Pred. No. 8.8e-06;
Matches 30; Conservative 16; Mismatches 34; Indels 8; Gaps 3;
```

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QY 16 GENVELKCOVLN--PTSGCSWLFQPGAAASPTFLYLSQNKPKAAEGLDTPREGGR 73
DB 15 GGSITTSCTGTSDDIGAYNVSWYQYPRGA--PKLLIYVSNRPSGI----SNRFGSK 68
QY 74 LGDTFVLTLSDFRRENGYFCSALNS 101
DB 69 SGPSTLISLGERATLSCRASQSVSSSYLAWYQQRGA--PRLLIY---GASRRATGI-P 60
```

```
RESULT 10
US-10-771-257-64
; Sequence 64, Application US/10771257
; Publication No. US2005028866A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: SISSA - Scuola Superiore Internazionale di Studi Avanzati
; APPLICANT: Cattaneo, Antonino
; APPLICANT: Maritan, Amos
; APPLICANT: Visintin, Michela
; APPLICANT: Rabbitts, Terrence H
; APPLICANT: Settanni, Giovanni
; TITLE OF INVENTION: Intracellular antibodies
; FILE REFERENCE: 18396/2272
; CURRENT APPLICATION NUMBER: US/10/771,257
; PRIOR FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: PCT/GB02/03512
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: GB 0119004.0
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: GB 0121577.1
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: GB 0200928.0
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: GB 0203569.9
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: IT RM2001A000633
; PRIOR FILING DATE: 2001-10-25
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-771-257-64
```

```
Query Match          18.5%; Score 119; DB 6; Length 109;
Best Local Similarity 35.9%; Pred. No. 8.8e-06;
Matches 33; Conservative 12; Mismatches 41; Indels 6; Gaps 3;
```

```
QY 7 SPIDRTWNLGETVELKCOVLNSPTSGCSWLFQPGAAASPTFLYLSQNKPKAAEGLDTP 66
DB 7 SPFTLISLGERATLSCRASQSVSSSYLAWYQQRGA--PRLLIY---GASRRATGI-P 60
QY 67 QRFSGKRLGDTFVLTLSDFRRENGYFCSAL 98
DB 61 DRFSGSGSGTDFLTITSLQPEDFGTYCCQL 92
```

```
RESULT 11
US-11-127-677-62
; Sequence 62, Application US/11127677
; Publication No. US20050272107A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Rabbitts, Terrence H
; APPLICANT: Tanaka, Tomoyuki
; TITLE OF INVENTION: Intracellular antibodies
; FILE REFERENCE: 18396/2462
; CURRENT APPLICATION NUMBER: US/11/127,677
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: PCT/GB03/04942
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: GB 0226729.2
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived protein sequence of scFv
US-11-127-677-62
```

```
Query Match          18.5%; Score 119; DB 7; Length 109;
Best Local Similarity 35.9%; Pred. No. 8.8e-06;
Matches 33; Conservative 12; Mismatches 41; Indels 6; Gaps 3;
```

```
QY 7 SPIDRTWNLGETVELKCOVLNSPTSGCSWLFQPGAAASPTFLYLSQNKPKAAEGLDTP 66
DB 7 SPFTLISLGERATLSCRASQSVSSSYLAWYQQRGA--PRLLIY---GASRRATGI-P 60
QY 67 QRFSGKRLGDTFVLTLSDFRRENGYFCSAL 98
DB 61 DRFSGSGSGTDFLTITSLQPEDFGTYCCQL 92
```

```
RESULT 12
US-10-952-535A-6
; Sequence 6, Application US/10952535A
; Publication No. US2005025513A1
; GENERAL INFORMATION:
; APPLICANT: Huxton, James S.
; APPLICANT: Messer, Anne
; APPLICANT: Lecert, Jean-Michel
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITTING POLYPEPTIDE
; TITLE OF INVENTION: ACCUMULATION ASSOCIATED WITH NEUROLOGICAL DISORDERS
; FILE REFERENCE: INR-004CP
; CURRENT APPLICATION NUMBER: US/10/952,535A
; PRIOR FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: 60/146,047
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: construct
US-10-952-535A-6

Query Match      18.5%; Score 119; DB 6; Length 239;
Best Local Similarity 34.1%; Pred. No. 2.1e-05;
Matches 30; Conservative 16; Mismatches 34; Indels 8; Gaps 3;

QY 16 GIVEYELKQVILSN--PTSGCSWLPQPGAAASPTFLYLSQNKPKAEGLDTPRSGKR 73
DB 145 GGSITISCTGTSDDIGAYNVSWYQYPGA--PKLLIDVSNRPSGI-----SNRFGSK 198
74 LGDTFVLTLSDPRRNEGYPFGSALSNS 101
DB 199 SGDTASLTISGLQAEDEADYTCSSPANS 226

RESULT 13
US-10-982-440-12
Sequence 12, Application US/10982440
Publication No. US20060018909A1
GENERAL INFORMATION:
APPLICANT: Olinet, John
APPLICANT: Graham, Kevin
TITLE OF INVENTION: Angiopoietin-2 Specific Binding Agents
FILE REFERENCE: 04-881-A
CURRENT APPLICATION NUMBER: US/10/982,440
PRIOR FILING DATE: 2004-11-04
PRIOR APPLICATION NUMBER: 60/620,161
NUMBER OF SEQ ID NOS: 215
SOFTWARE: PatentIn version 3.3
SEQ ID NO 12
LENGTH: 112
TYPE: PRT
ORGANISM: Homo sapiens
US-10-982-440-12

Query Match      18.5%; Score 118.5; DB 6; Length 112;
Best Local Similarity 32.7%; Pred. No. 1e-05;
Matches 36; Conservative 12; Mismatches 45; Indels 17; Gaps 5;

QY 7 SPLDRTWNLGEYELKQV-----VLISNPTSGCSWLPQPGAAASPTFLYLSQNKPKA 62
DB 7 SPLSLPVTGEPASISCRSSQSLHNSGNVLDWYQKPC--QSPQLLYLGSNR---AS 61
QY 63 GUDTORFSGKRLGDTFVLTLSDPRRNEGYPFGSALSNSIMYPSHFVPPV 112
DB 62 GY-PDRFSGSGSGTDFTLKISRVEADVGVYTC-----MGCTHWPPTF 103

RESULT 14
US-10-512-184-27
Sequence 27, Application US/10512184
Publication No. US20050244901A1
GENERAL INFORMATION:
APPLICANT: Fraunhofer Gesellschaft zur F"orderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
FILE REFERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 27
LENGTH: 250
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: scFv SGB3 with
OTHER INFORMATION: specificity against Pseudium ssp.; originates from
```

```
OTHER INFORMATION: Gallus gallus.
US-10-512-184-27

Query Match      18.5%; Score 118.5; DB 7; Length 250;
Best Local Similarity 32.6%; Pred. No. 2.5e-05;
Matches 29; Conservative 14; Mismatches 37; Indels 9; Gaps 3;

QY 14 NIGEYELKQVILSNPTSGCSWLPQPGAAASPTFLYLSQNKPKAEGLDTPRSGKR 73
DB 154 NLGQTYKATC-----SSSTHYHGW-HQOKSPGSAFVTLISFNNQRPEDI-----PSRFGSK 204
74 LGDTFVLTLSDPRRNEGYPFGSALSNSI 102
DB 205 SGSTGTTLITGVAEDEADVYTCGMDRST 233

RESULT 15
US-11-054-515-1833
Sequence 1833, Application US/11054515
Publication No. US2005025532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: P5523P3
CURRENT APPLICATION NUMBER: US/11/054,515
PRIOR FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1833
LENGTH: 251
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-1833

Query Match      18.5%; Score 118.5; DB 7; Length 251;
Best Local Similarity 33.0%; Pred. No. 2.5e-05;
Matches 31; Conservative 14; Mismatches 28; Indels 21; Gaps 4;

QY 15 LGEYELKQVILSNPTSG-----CSWLPQPGAAASPTFLYLSQNKPKAEGLDTPQ 67
DB 156 LGQTYITICQ-----GDSVRFYASWYQKPCQA--PLLVITGQNNRPSGI-----PD 201
QY 68 RPSGKRLGDTFVLTLSDPRRNEGYPFGSALSNS 101
DB 202 RPSGSGSNTASLTITGAQAEDEGVYTCNSRDS 235
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Search completed: April 5, 2006, 16:04:18
Job time : 26 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: April 5, 2006, 15:54:16 ; Search time 43 Seconds

(without alignments)
1175.752 Million cell updates/sec

Title: US-09-560-494E-24

Perfect score: 642
Sequence: 1 MSQFRVSPIDRTWNLGRTVE.....IMYFSPVFPVLPKPTTTP 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:
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2: /cgn2_6/ptodata/1/pubpaa/us08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/us09_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/us11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	637	99.2	198	US-10-804-762-3	Sequence 3, Appl1
2	637	99.2	198	US-10-804-763-3	Sequence 3, Appl1
3	637	99.2	218	US-10-378-393-20	Sequence 20, Appl1
4	637	99.2	219	US-10-378-393-3	Sequence 3, Appl1
5	637	99.2	219	US-10-378-393-13	Sequence 13, Appl1
6	637	99.2	235	US-10-099-007A-6	Sequence 6, Appl1
7	637	99.2	235	US-10-207-655-174	Sequence 174, App
8	637	99.2	235	US-10-723-860-1244	Sequence 1244, App
9	637	99.2	235	US-10-804-762-1	Sequence 1, Appl1
10	637	99.2	235	US-10-804-762-27	Sequence 27, Appl1
11	637	99.2	235	US-10-804-763-1	Sequence 1, Appl1
12	637	99.2	624	US-10-378-393-7	Sequence 7, Appl1
13	637	99.2	646	US-10-378-393-18	Sequence 18, Appl1
14	637	99.2	791	US-10-378-393-11	Sequence 11, Appl1
15	629	98.0	197	US-10-804-762-32	Sequence 32, Appl1
16	629	98.0	197	US-10-804-763-51	Sequence 51, Appl1
17	602	93.8	235	US-10-804-763-27	Sequence 27, Appl1
18	599	93.3	198	US-10-804-762-5	Sequence 5, Appl1
19	599	93.3	198	US-10-804-763-5	Sequence 5, Appl1
20	547	85.2	235	US-10-804-763-25	Sequence 25, Appl1
21	547	85.2	235	US-10-804-763-25	Sequence 25, Appl1
22	536	83.5	102	US-09-891-119A-13	Sequence 13, Appl1
23	366.5	57.1	239	US-10-804-762-21	Sequence 21, Appl1
24	366.5	57.1	239	US-10-804-763-21	Sequence 21, Appl1
25	362	56.4	236	US-10-804-762-19	Sequence 19, Appl1
26	362	56.4	236	US-10-804-763-19	Sequence 19, Appl1
27	347.5	54.1	242	US-10-804-762-17	Sequence 17, Appl1

28	347.5	54.1	242	5	US-10-804-763-17	Sequence 17, Appl1
29	340	53.0	237	5	US-10-804-762-15	Sequence 15, Appl1
30	340	53.0	237	5	US-10-804-763-15	Sequence 15, Appl1
31	279.5	43.5	235	5	US-10-804-762-23	Sequence 23, Appl1
32	279.5	43.5	235	5	US-10-804-763-23	Sequence 23, Appl1
33	248	38.6	236	5	US-10-804-762-13	Sequence 13, Appl1
34	248	38.6	236	5	US-10-804-763-13	Sequence 13, Appl1
35	239	37.2	310	5	US-10-804-762-7	Sequence 7, Appl1
36	239	37.2	310	5	US-10-804-763-7	Sequence 7, Appl1
37	238	37.1	247	5	US-10-804-762-11	Sequence 11, Appl1
38	238	37.1	247	5	US-10-804-762-31	Sequence 31, Appl1
39	238	37.1	247	5	US-10-804-763-11	Sequence 11, Appl1
40	238	37.1	247	5	US-10-804-763-50	Sequence 50, Appl1
41	232	36.1	207	5	US-10-804-762-9	Sequence 9, Appl1
42	232	36.1	207	5	US-10-804-763-9	Sequence 9, Appl1
43	229	35.7	310	5	US-10-804-762-29	Sequence 29, Appl1
44	229	35.7	310	5	US-10-804-763-29	Sequence 29, Appl1
45	139	21.7	444	2	US-08-812-393A-2	Sequence 2, Appl1

ALIGNMENTS

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RESULT 1
US-10-804-762-3
; Sequence 3, Application US/10804762
; Publication No. US20050042217A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Yan
; APPLICANT: Zhang, Xianghua
; APPLICANT: Konigsberg, Paula
; TITLE OF INVENTION: Specific Inhibition of Allotransplantation
; FILE REFERENCE: A-72186/TAL/DCP (471702-00005)
; CURRENT APPLICATION NUMBER: US/10/804,762
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/456,378
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-804-762-3

Query Match          99.2%; Score 637; DB 5; Length 198;
Best Local Similarity 100.0%; Pred. No. 3e-60;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  SQFRVSPIDRTWNLGRTVEIKQVLLSNPTSGCSWLFORGAASFTPLLYISQNKPKKA 61
      |||
DB      22  SQFRVSPIDRTWNLGRTVEIKQVLLSNPTSGCSWLFORGAASFTPLLYISQNKPKKA 81
      |||

QY      62  EGLDTRFSGKRLGDFVTLTSPFRRENGYFCSALNSIMYFSPVFPVLPKPTTTP 121
      |||
DB      82  EGLDTRFSGKRLGDFVTLTSPFRRENGYFCSALNSIMYFSPVFPVLPKPTTTP 141
      |||

RESULT 2
US-10-804-763-3
; Sequence 3, Application US/10804763
; Publication No. US20050118676A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Yan
; APPLICANT: Zhang, Xianghua
; APPLICANT: Konigsberg, Paula
; TITLE OF INVENTION: Gene Therapy Vectors Having Reduced Immunogenicity
; FILE REFERENCE: A-72186-1/TAL/DCP (471702-00008)
; CURRENT APPLICATION NUMBER: US/10/804,763
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/456,378
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 51

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SOFTWARE: PatentIn Ver 2.0
SEQ ID NO 6
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-10-099-007A-6

Query Match 99.2%; Score 637; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.6e-60;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQRVSPDLRTWNLGETVELKCOVLNSPTSGCSWLFQPRGAASPTFLYLTSQNKPKAA 61
DB 22 SQRVSPDLRTWNLGETVELKCOVLNSPTSGCSWLFQPRGAASPTFLYLTSQNKPKAA 81
DB 62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCALSNSIMYFSHFVPLPAKPTTTP 121
82 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCALSNSIMYFSHFVPLPAKPTTTP 141

RESULT 7

US-10-207-655-174
Sequence 174, Application US/10207655
Publication No. US20030118592A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 39069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
NUMBER OF SEQ ID NOS: 426
SOFTWARE: PatentIn version 3.0
SEQ ID NO 174
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-10-207-655-174

Query Match 99.2%; Score 637; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.6e-60;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQRVSPDLRTWNLGETVELKCOVLNSPTSGCSWLFQPRGAASPTFLYLTSQNKPKAA 61
DB 22 SQRVSPDLRTWNLGETVELKCOVLNSPTSGCSWLFQPRGAASPTFLYLTSQNKPKAA 81
QY 62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCALSNSIMYFSHFVPLPAKPTTTP 121
DB 82 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCALSNSIMYFSHFVPLPAKPTTTP 141

RESULT 8

US-10-723-860-1244
Sequence 1244, Application US/10723860
Publication No. US20040253606A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
FILE REFERENCE: 05882.0193 NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1244
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens

US-10-723-860-1244

Query Match 99.2%; Score 637; DB 5; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.6e-60;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 22 SQRVSPDLRTWNLGETVELKCOVLNSPTSGCSWLFQPRGAASPTFLYLTSQNKPKAA 81
QY 62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCALSNSIMYFSHFVPLPAKPTTTP 121
DB 82 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCALSNSIMYFSHFVPLPAKPTTTP 141

RESULT 9

US-10-804-762-1
Sequence 1, Application US/10804762
Publication No. US20050042217A1
GENERAL INFORMATION:
APPLICANT: Qi, Yan
APPLICANT: Zhang, Xianghua
APPLICANT: Konigsberg, Paula
TITLE OF INVENTION: Specific Inhibition of Allotransplantation
FILE REFERENCE: A-72186/TAL/DCF (471702-00005)
CURRENT APPLICATION NUMBER: US/10/804,762
CURRENT FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: US 60/456,378
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-10-804-762-1

Query Match 99.2%; Score 637; DB 5; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.6e-60;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQRVSPDLRTWNLGETVELKCOVLNSPTSGCSWLFQPRGAASPTFLYLTSQNKPKAA 61
DB 22 SQRVSPDLRTWNLGETVELKCOVLNSPTSGCSWLFQPRGAASPTFLYLTSQNKPKAA 81
QY 62 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCALSNSIMYFSHFVPLPAKPTTTP 121
DB 82 EGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCALSNSIMYFSHFVPLPAKPTTTP 141

RESULT 10

US-10-804-762-27
Sequence 27, Application US/10804762
Publication No. US20050042217A1
GENERAL INFORMATION:
APPLICANT: Qi, Yan
APPLICANT: Zhang, Xianghua
APPLICANT: Konigsberg, Paula
TITLE OF INVENTION: Specific Inhibition of Allotransplantation
FILE REFERENCE: A-72186/TAL/DCF (471702-00005)
CURRENT APPLICATION NUMBER: US/10/804,762
CURRENT FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: US 60/456,378
PRIOR FILING DATE: 2003-03-19
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.2
SEQ ID NO 27
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-10-804-762-27

Query Match 99.2%; Score 637; DB 5; Length 235;

Best Local Similarity 100.0%; Pred. No. 3.6e-60;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2	SOFRUSPLDRTMNLGETYVLELKCOVILSNSTSGSMT.PORPGAASPTFLIYLXSONPKKA	61
Db	22	SOFRUSPLDRTMNLGETYVLELKCOVILSNSTSGSMT.PORPGAASPTFLIYLXSONPKKA	81
Qy	62	EGLDTORPSGKRLGDTFVLTLLSDFRRENGEYFCSALSNISIMYFSHPVFPVFLPAKPTTTP	121
Db	82	EGLDTORPSGKRLGDTFVLTLLSDFRRENGEYFCSALSNISIMYFSHPVFPVFLPAKPTTTP	141

RESULT 11

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US-10-804-763-1
: Sequence 1, Application US/10804763
: Publication No. US20050118676A1
: GENERAL INFORMATION:
: APPLICANT: Qi, Yan
: APPLICANT: Zhang, Xianghua
: APPLICANT: Konigsberg, Paula
: TITLE OF INVENTION: Gene Therapy Vectors Having Reduced Immunogenicity
: FILE REFERENCE: A-72186-1/TAL/DCP (471702-00008)
: CURRENT APPLICATION NUMBER: US/10/804,763
: CURRENT FILING DATE: 2004-03-19
: PRIOR APPLICATION NUMBER: US 60/456,378
: PRIOR FILING DATE: 2003-03-19
: NUMBER OF SEQ ID NOS: 51
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 1
: LENGTH: 235
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-804-763-1

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Query Match	99.2%	Score 637	DB 5	Length 235
Best Local Similarity	100.0%	Pred. No. 3.6e-60		
Matches 120	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	Db	QY
2	2	61
2	22	81
62	62	121
82	82	141

RESULT 12

US-10-378-393-7
Sequence 7, Application US/10378393
Publication NO. US2003018268A1
GENERAL INFORMATION:
APPLICANT: Bol, David K.
APPLICANT: Cardoni, Joan M.
APPLICANT: Rowley, Ronald B.
APPLICANT: Wong, Tai W.
APPLICANT: Lee, Francis Y.
TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
TITLE OF INVENTION: TYROSINE KINASE RECEPTORS
FILE REFERENCE: D0254 NP
CURRENT APPLICATION NUMBER: US/10/378,393
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/360,889
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.2
SEQ ID NO 7
LENGTH: 624
TYPE: PRT
ORGANISM: Homo sapiens
US-10-378-393-7

Query Match 99.2%; Score 637; DB 4; Length 624;

Best Local Similarity 100.0%; Pred. No. 1.le-59;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQRVSEPLRTNNIGETVEIKCOVLTLSNPTSGSCMLPQPGAAASPFLILYYSQNKPKA 61

Db 22 SQRVSEPLRTNNIGETVEIKCOVLTLSNPTSGSCMLPQPGAAASPFLILYYSQNKPKA 81

QY 62 EGLDTRFSGKRLGDTFVLTLSDFPRENENGYFCSALSNISIMVSHFVVPFLPAKPTTTP 121

Db 82 EGLDTRFSGKRLGDTFVLTLSDFPRENENGYFCSALSNISIMVSHFVVPFLPAKPTTTP 141

RESULT 13

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US-10-378-393-18
; Sequence 18, Application US/10378393
; Publication No. US20030182668A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TYRASENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
; TITLE OF INVENTION: TYROSINE KINASE RECEPTORS
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,889
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-378-393-18

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Query Match      99.2%; Score 637; DB 4; Length 646;
Best Local Similarity 100.0%; Pred. No. 1.2e-59;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 SQRVSRPLRTNMGHTVELKQVLTLSPTSGCSMLRPPGRGAAASPPELLYLSGNPKKA 61

Db 22 SQRVSRPLRTNMGHTVELKQVLTLSPTSGCSMLRPPGRGAAASPPELLYLSGNPKKA 81

QY 62 EGLDTRFSQKRLGDTFVLTSLSPRRNEGYFFCSALSNLSIMYSHFVFWFLPAKPTTP 121

Db 82 EGLDTRFSQKRLGDTFVLTSLSPRRNEGYFFCSALSNLSIMYSHFVFWFLPAKPTTP 141

RESULT 14
US-10-378-393-11

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? Sequence ID: Application US/10378393
? Publication No. US20030182668A1
? GENERAL INFORMATION:
? APPLICANT: Bol, David K.
? APPLICANT: Carbont, Joan M.
? APPLICANT: Rowley, Ronald B.
? APPLICANT: Wong, Tai W.
? APPLICANT: Lee, Francis Y.
? TITLE OF INVENTION: TYROSINE KINASE RECEPTORS
? TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
? FILE REFERENCE: D0254 NP
? CURRENT APPLICATION NUMBER: US/10/378,393
? CURRENT FILING DATE: 2003-03-03
? PRIOR APPLICATION NUMBER: US 60/360,889
? PRIOR FILING DATE: 2002-03-01
? NUMBER OF SEQ ID NOS: 23
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO 11
? LENGTH: 791
? TYPE: prt
? ORGANISM: Homo sapiens

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US-10-378-393-11

Query Match	99.2%	Score 637	DB 4	Length 791
Best Local Similarity	100.0%	Pred. No.	1	Se-59
Matches 120; Conservative	0;	Mismatches	0;	Gaps 0

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Db	22	SGRVAPLRLTNVLGSEIVELKCVLLSNTPSGCSNLPQVRGAAPLPTLLVLSQNKPRAA	81
QY	62	EGSLDTRFSGKRLGDPFVLTLDPRRNGGYFCSALSNLSINYSFHNPVPLPAKPTTPP	121
Db	82	EGSLDTRFSGKRLGDPFVLTLDPRRNGGYFCSALSNLSINYSFHNPVPLPAKPTTPP	141

RESULT 15
TIS-10-804

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US-10-804-762-32
Sequence 32, Application US/10804762
Publication NO. US2005004217A1
GENERAL INFORMATION:
APPLICANT: Qi, Yan
APPLICANT: Zhang, Xianghua
APPLICANT: Konigsberg, Paula
TITLE OF INVENTION: Specific Inhibition of Allotransjection
FILE REFERENCE: A-721867/AL/DCF (471702-00005)
CURRENT APPLICATION NUMBER: US/10/804,762
PRIORITY FILING DATE: 2004-03-19
PRIOR FILING DATE: 2003-03-19
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.2
SEQ ID NO 32
LENGTH: 197
TYPE: PRT
ORGANISM: Homo sapiens
US-10-804-762-32

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Query Match	98.0%	Score 629	DB 5	length 197
Best Local Similarity	99.2%	Pred. No. 2.1e-59		
Matches 119	Conservative	0	Mismatches 1	Indels 0
			Gaps	0

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Search completed: April 5, 2006, 15:55:07
Job time : 44 secs

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GenCore version 5.1.7
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Run on: April 5, 2006, 15:52:51 ; Search time 19 Seconds

(without alignments)
526.514 Million cell updates/sec

Title: US-09-560-494E-24

Perfect score: 642
Sequence: 1 MSQFRVSPIDRTWNLGRTVE.....IMYFHPVPLPAKPTTP 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
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Database :

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3: /cgn2_6/prodata/1/1aa/H COMB.dep:*
4: /cgn2_6/prodata/1/1aa/PCBUS COMB.dep:*
5: /cgn2_6/prodata/1/1aa/RX COMB.dep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	637	99.2	235	1	US-07-940-605A-12
2	637	99.2	235	1	US-08-690-096-12
3	637	99.2	235	1	US-08-751-512-8
4	603	93.9	114	1	US-08-372-952-1
5	603	93.9	114	2	US-08-875-309-1
6	603	93.9	114	4	PCT-US96-00310-1
7	603	93.9	114	1	Sequence 1, Appl
8	536	83.5	102	2	US-08-403-853-12
9	536	83.5	102	2	US-08-466-368-8
10	536	83.5	102	2	US-08-470-998-5
11	239	37.2	249	1	US-07-940-605A-10
12	239	37.2	249	1	US-08-690-096-10
13	228	35.5	280	1	US-08-403-853-10
14	227.5	35.4	269	2	US-09-531-056A-13
15	227.5	35.4	328	2	US-09-531-056A-13
16	227.5	35.4	331	2	US-09-531-056A-12
17	135.5	21.1	124	2	US-08-751-359-14
18	135.5	21.1	124	2	US-08-907-146-14
19	127.5	19.9	105	2	US-10-083-424-30
20	120.5	18.8	126	2	US-10-083-424-30
21	120.5	18.8	126	2	US-08-751-359-12
22	119.5	18.6	235	2	US-09-049-672A-10
23	119.5	18.6	108	2	US-09-814-695-34
24	117.5	18.3	229	2	US-08-751-359-22
25	117.5	18.3	229	2	US-08-751-359-22
26	117.5	18.3	229	2	US-08-907-146-22
27	115.5	18.0	104	2	US-10-083-424-40

28	113	17.6	104	2	US-10-083-424-28	Sequence 28, Appl
29	113	17.6	112	2	US-10-330-613A-2	Sequence 2, Appl
30	111.5	17.4	108	2	US-10-092-246-19	Sequence 19, Appl
31	111.5	17.4	108	2	US-10-096-246A-19	Sequence 19, Appl
32	111.5	17.4	111	1	US-08-665-202-36	Sequence 36, Appl
33	111.5	17.4	111	1	US-09-315-574-36	Sequence 36, Appl
34	111.5	17.4	113	2	US-09-232-290-20	Sequence 20, Appl
35	111.5	17.4	258	1	US-08-665-202-5	Sequence 5, Appl
36	111.5	17.4	258	1	US-09-315-574-5	Sequence 5, Appl
37	111.5	17.4	262	2	US-09-069-821-4	Sequence 4, Appl
38	111.5	17.4	262	2	US-09-956-086-4	Sequence 4, Appl
39	111.5	17.4	262	2	US-09-956-087-4	Sequence 4, Appl
40	111.5	17.4	282	2	US-09-420-592A-7	Sequence 7, Appl
41	111.5	17.4	282	2	US-09-985-442-7	Sequence 7, Appl
42	111.5	17.4	282	2	US-09-983-580-7	Sequence 7, Appl
43	111	17.3	130	2	US-09-339-596A-28	Sequence 28, Appl
44	110.5	17.2	106	2	US-09-240-274-47	Sequence 47, Appl
45	110.5	17.2	106	2	US-09-848-798-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1
US-07-940-605A-12

Sequence 12, Application US/07940605A
Patent No. 5540926

GENERAL INFORMATION:

APPLICANT: ARUPPO, ALEJANDRO

APPLICANT: HOLLENBAUGH, DIANE

TITLE OR INVENTION: SOLUBLE LIGANDS FOR CD40

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESS: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/940,605A

FILING DATE: 04-SEP-1992

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Mastrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 5624-184

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 790-9090

TELEFAX: 212 869-8864/9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 235 amino acids

TYPE: amino acids

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-07-940-605A-12

Query Match 99.2%; Score 637; DB 1; Length 235;

Best local similarity 100.0%; Pred. No. 4.8e-64;

Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQFRVSPIDRTWNLGRTVEIKCVILSNFTSGCSWIFQPRGAASPTFLIYSQNKPKAA 61
DB 22 SQFRVSPIDRTWNLGRTVEIKCVILSNFTSGCSWIFQPRGAASPTFLIYSQNKPKAA 81

QY 62 EGI DTORFSGKRLGDTFVLTLSDFRRENEGYYFCALSINSIMYFSHFVVPFLPAKPTTTP 121
DB 82 EGI DTORFSGKRLGDTFVLTLSDFRRENEGYYFCALSINSIMYFSHFVVPFLPAKPTTTP 141

RESULT 2

US-08-690-096-12
Sequence 12, Application US/08690096
Patent No. 5945513
GENERAL INFORMATION:
APPLICANT: ARUFFO, ALEJANDRO
APPLICANT: HOLLENBAUGH, DIANE
APPLICANT: LEDBETTER, JEFFREY A.
TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: Penite & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,096
FILING DATE: 31-JUL-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/940,605
FILING DATE: 04-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mierock, S. Leslie
REGISTRATION NUMBER: 18,672
REFERENCE/DOCKET NUMBER: 5624-184
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-690-096-12

Query Match 99.2%; Score 637; DB 1; Length 235;
Best Local Similarity 100.0%; Pred. No. 4.8e-64;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQFRVSPLDRTWNLGETVETLKCVLLSNPTSGCSWLPQPRGAASPTFLIYSQNKPKKA 61
DB 22 SQFRVSPLDRTWNLGETVETLKCVLLSNPTSGCSWLPQPRGAASPTFLIYSQNKPKKA 81
QY 62 EGI DTORFSGKRLGDTFVLTLSDFRRENEGYYFCALSINSIMYFSHFVVPFLPAKPTTTP 121
DB 82 EGI DTORFSGKRLGDTFVLTLSDFRRENEGYYFCALSINSIMYFSHFVVPFLPAKPTTTP 141

RESULT 3

US-08-751-512-8
Sequence 8, Application US/08751512
Patent No. 6001962
GENERAL INFORMATION:
APPLICANT: Ramer, J. Kevin
APPLICANT: Williams, Lewis T.
TITLE OF INVENTION: Modified PAS Ligands
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:

ADDRESSER: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,512
FILING DATE: 15-NOV-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, Matthew B.
REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 02307K-07100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-751-512-8

Query Match 99.2%; Score 637; DB 2; Length 376;
Best Local Similarity 100.0%; Pred. No. 8.8e-64;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQFRVSPLDRTWNLGETVETLKCVLLSNPTSGCSWLPQPRGAASPTFLIYSQNKPKKA 61
DB 22 SQFRVSPLDRTWNLGETVETLKCVLLSNPTSGCSWLPQPRGAASPTFLIYSQNKPKKA 81
QY 62 EGI DTORFSGKRLGDTFVLTLSDFRRENEGYYFCALSINSIMYFSHFVVPFLPAKPTTTP 121
DB 82 EGI DTORFSGKRLGDTFVLTLSDFRRENEGYYFCALSINSIMYFSHFVVPFLPAKPTTTP 141

RESULT 4

US-08-372-952-1
Sequence 1, Application US/08372952
Patent No. 5645837
GENERAL INFORMATION:
APPLICANT: Jameson, Bradford A.
APPLICANT: Chokel, Swael
APPLICANT: Korngold, Robert
TITLE OF INVENTION: CD8 Antagonists
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSER: No. 564583718
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/372,952
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1440
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-372-952-1

Query Match 93.9%; Score 603; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.3e-60;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQRVSPDLRTWNLGETVETLKQVLLSNPTSGCSWLFQPRGAASPFTLLYLSQNKPKAA 61
DB 1 SQRVSPDLRTWNLGETVETLKQVLLSNPTSGCSWLFQPRGAASPFTLLYLSQNKPKAA 60

QY 62 EGLDTQRFSGKRLGDTFVLTLSDFRRNKGYYFCALSNSIMYFSHPVPLPA 115
DB 61 EGLDTQRFSGKRLGDTFVLTLSDFRRNKGYYFCALSNSIMYFSHPVPLPA 114

RESULT 5
US-08-875-309-1
Sequence 1, Application US/08875309
Patent No. 6180600
GENERAL INFORMATION:
APPLICANT: Jameson, Bradford A.
APPLICANT: Choksi, Swati
APPLICANT: Korgold, Robert
APPLICANT: Huang, Ziwei
TITLE OF INVENTION: CD8 Antagonists
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 61806000ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,309
FILING DATE: 26-NOV-1997
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00310
FILING DATE: 17-JAN-1996
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/372,952
FILING DATE: 17-JAN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1772
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 114 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-309-1

Query Match 93.9%; Score 603; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.3e-60;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQRVSPDLRTWNLGETVETLKQVLLSNPTSGCSWLFQPRGAASPFTLLYLSQNKPKAA 61
DB 1 SQRVSPDLRTWNLGETVETLKQVLLSNPTSGCSWLFQPRGAASPFTLLYLSQNKPKAA 60

QY 62 EGLDTQRFSGKRLGDTFVLTLSDFRRNKGYYFCALSNSIMYFSHPVPLPA 115
DB 61 EGLDTQRFSGKRLGDTFVLTLSDFRRNKGYYFCALSNSIMYFSHPVPLPA 114

RESULT 6
PCT-US96-00310-1
Sequence 1, Application PC/TUS9600310
GENERAL INFORMATION:
APPLICANT: Jameson, Bradford A.
APPLICANT: Choksi, Swati
APPLICANT: Korgold, Robert
APPLICANT: Huang, Ziwei
TITLE OF INVENTION: CD8 Antagonists
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00310
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/372,952
FILING DATE: 17-JAN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1752
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-00310-1

Query Match 93.9%; Score 603; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.3e-60;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQRVSPDLRTWNLGETVETLKQVLLSNPTSGCSWLFQPRGAASPFTLLYLSQNKPKAA 61
DB 1 SQRVSPDLRTWNLGETVETLKQVLLSNPTSGCSWLFQPRGAASPFTLLYLSQNKPKAA 60

QY 62 EGLDTQRFSGKRLGDTFVLTLSDFRRNKGYYFCALSNSIMYFSHPVPLPA 115

Db 61 EGIIDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCALSINSIMYFSHFVPLPA 114

RESULT 7
US-08-403-853-12

/ Sequence 12, Application US/08403853
/ Patent No. 5844094
/ GENERAL INFORMATION:
/ APPLICANT: HUDSON, Peter J.
/ APPLICANT: LAH, Maria
/ APPLICANT: KORRT, Alex A.
/ APPLICANT: IRVING, Robert A.
/ APPLICANT: ATWELL, John L.
/ APPLICANT: MALBY, Robyn L.
/ APPLICANT: POWER, Barbara E.
/ APPLICANT: COLMAN, Peter M.
/ TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
/ NUMBER OF SEQUENCES: 25
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Foley & Lardner
/ STREET: 3000 K Street, N.W., Suite 500
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20007-5109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/403,853
/ FILING DATE: 30-MAY-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: WO PCT/AU93/00491
/ FILING DATE: 24-SEP-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: AU PL 4973
/ FILING DATE: 25-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BENT, Stephen A.
/ REGISTRATION NUMBER: 29,768
/ REFERENCE/DOCKET NUMBER: 16786/189/CHAC
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)672-5300
/ TELEFAX: (202)672-5399
/ TELEX: 904136
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 273 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-403-853-12

Query Match 93.9%; Score 603; DB 1; length 273;
Best local Similarity 100.0%; Pred. No. 4.1e-60;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQFRVSPIDRTWNLGETVELKQVLLSNPTSGCSWLFQPRGAASPTFLIYLSQNKPKAA 61
DB 23 SQFRVSPIDRTWNLGETVELKQVLLSNPTSGCSWLFQPRGAASPTFLIYLSQNKPKAA 82
QY 62 EGIIDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCALSINSIMYFSHFVPLPA 115
DB 83 EGIIDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCALSINSIMYFSHFVPLPA 136

RESULT 8
US-08-466-368-8
/ Sequence 8, Application US/08466368

/ Patent No. 6093539
/ GENERAL INFORMATION:
/ APPLICANT: Maddon, Paul J.
/ APPLICANT: Littman, Dan R.
/ APPLICANT: Chess, Leonard
/ APPLICANT: Axel, Richard
/ APPLICANT: Weiss, Robin
/ APPLICANT: McDougal, J. S.
/ TITLE OF INVENTION: DNA ENCODING THE T CELL SURFACE PROTEIN
/ NUMBER OF SEQUENCES: 21
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Cooper & Dunham LLP
/ STREET: 1185 Avenue of Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/466,368
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: White, John P.
/ REGISTRATION NUMBER: 28,678
/ REFERENCE/DOCKET NUMBER: 24577-E1-B/DW/AKC
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 212-278-0400
/ TELEFAX: 212-391-0525
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 102 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: YES
/ ANTI-SENSE: YES
/ FEATURE:
/ NAME/KEY: Active-site
/ LOCATION: 1..102
/ US-08-466-368-8

Query Match 83.5%; Score 536; DB 2; length 102;
Best local Similarity 100.0%; Pred. No. 4.4e-53;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQFRVSPIDRTWNLGETVELKQVLLSNPTSGCSWLFQPRGAASPTFLIYLSQNKPKAA 61
DB 1 SQFRVSPIDRTWNLGETVELKQVLLSNPTSGCSWLFQPRGAASPTFLIYLSQNKPKAA 60
QY 62 EGIIDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCALSINSIM 103
DB 61 EGIIDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCALSINSIM 102

RESULT 9
US-08-470-998-5
/ Sequence 5, Application US/08470998
/ Patent No. 6570000
/ GENERAL INFORMATION:
/ APPLICANT: Maddon, Paul J.
/ APPLICANT: Littman, Dan R.
/ APPLICANT: Chess, Leonard
/ APPLICANT: Axel, Richard
/ APPLICANT: Weiss, Robin
/ APPLICANT: McDougal, J. S.
/ TITLE OF INVENTION: DNA ENCODING THE T CELL SURFACE PROTEIN

TITLE OF INVENTION: T4 AND USE OF FRAGMENTS OF T4 IN THE TREATMENT OF AIDS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,998
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 24577-P1-B/JPM/AKC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: protein
HYPOTHEICAL: YES
ANTI-SENSE: YES
FEATURE:
NAME/KEY: Active-site
LOCATION: 1..102
US-08-470-998-5

Query Match 83.5%; Score 536; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 4,4e-53;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SGRVSPPLDRTWNLGTEVETKCVLLSNPTSGCSWLFQPRGAASPTFLIYLSQNTPKAA 61
DB 1 SGRVSPPLDRTWNLGTEVETKCVLLSNPTSGCSWLFQPRGAASPTFLIYLSQNTPKAA 60

QY 62 EGIIDTQRFSGKRLGDTFVLTLSDFRRENEGYFCSALNSIM 103
DB 61 EGIIDTQRFSGKRLGDTFVLTLSDFRRENEGYFCSALNSIM 102

RESULT 10
US-08-328-500-13
Sequence 13, Application US/08328500
Patent No. 6673896
GENERAL INFORMATION:
APPLICANT: Maddon, Paul J.
APPLICANT: Axel, Richard
APPLICANT: Sweet, Richard W.
APPLICANT: Arthoe, James
TITLE OF INVENTION: DERIVATIVES OF SOLUBLE T-4
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,500
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/24577-CY
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULAR TYPE: protein
US-08-328-500-13

Query Match 83.5%; Score 536; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 4,4e-53;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SGRVSPPLDRTWNLGTEVETKCVLLSNPTSGCSWLFQPRGAASPTFLIYLSQNTPKAA 61
DB 1 SGRVSPPLDRTWNLGTEVETKCVLLSNPTSGCSWLFQPRGAASPTFLIYLSQNTPKAA 60

QY 62 EGIIDTQRFSGKRLGDTFVLTLSDFRRENEGYFCSALNSIM 103
DB 61 EGIIDTQRFSGKRLGDTFVLTLSDFRRENEGYFCSALNSIM 102

RESULT 11
US-07-940-605A-10
Sequence 10, Application US/07940605A
Patent No. 5540926
GENERAL INFORMATION:
APPLICANT: ARUFFO, ALEJANDRO
APPLICANT: HOLLENBAUGH, DIANE
APPLICANT: LEDBETTER, JEFFREY A.
TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/940,605A
FILING DATE: 04-SEP-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Mastro, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-184
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-940-605A-10

Query Match 37.2%; Score 239; DB 1; Length 249;
Best Local Similarity 44.7%; Pred. No. 5.5e-19;
Matches 55; Conservative 20; Mismatches 42; Indels 6; Gaps 5;

QY 3 QRVSPDLRTWNLGRTVELKCOVLTLSNPTSGCSWLPQPRGA-AASPTFLYL--SONKPK 59
DB 33 ELRIFFPKMDAELGQKVDLVCEV-LGSVSGCSWLPQNSSKLPQPTFVVYMASSHNKIT 91
QY 60 AAEGLDTR-FSGKR-LGDTFVLTLSDFRRENGYFCSALNSIMYFSHFVPLPAKP 117
DB 92 WDEKLNSSKLFAMRDNTNKKVLTINKFSKENEGYFCSVLSNVMYFSVVPVLQKVS 151
QY 118 TTT 120
DB 152 TTT 154

RESULT 12

US-08-690-096-10
Sequence 10, Application US/08690096
Patent No. 5945513

GENERAL INFORMATION:
APPLICANT: ARUPFO, ALEJANDRO
APPLICANT: HOLLENBAUGH, DIANE
APPLICANT: LEDBETTER, JEFFREY A.
TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,096
FILING DATE: 31-JUL-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/940,605
FILING DATE: 04-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mierock, S. Leslie
REGISTRATION NUMBER: 18,872
REPERENCE/DOCKET NUMBER: 5624-184
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-690-096-10

Query Match 37.2%; Score 239; DB 1; Length 249;
Best Local Similarity 44.7%; Pred. No. 5.5e-19;
Matches 55; Conservative 20; Mismatches 42; Indels 6; Gaps 5;

QY 3 QRVSPDLRTWNLGRTVELKCOVLTLSNPTSGCSWLPQPRGA-AASPTFLYL--SONKPK 59
DB 33 ELRIFFPKMDAELGQKVDLVCEV-LGSVSGCSWLPQNSSKLPQPTFVVYMASSHNKIT 91

QY 60 AAEGLDTR-FSGKR-LGDTFVLTLSDFRRENGYFCSALNSIMYFSHFVPLPAKP 117
DB 92 WDEKLNSSKLFAMRDNTNKKVLTINKFSKENEGYFCSVLSNVMYFSVVPVLQKVS 151

QY 118 TTT 120
DB 152 TTT 154

RESULT 13

US-08-403-853-10
Sequence 10, Application US/08403853
Patent No. 5844094

GENERAL INFORMATION:
APPLICANT: HUDSON, Peter J.
APPLICANT: KORRT, Alex A.
APPLICANT: IRVING, Robert A.
APPLICANT: ATWELL, John L.
APPLICANT: MALBY, Robyn L.
APPLICANT: POWER, Barbara E.
APPLICANT: COLMAN, Peter M.
TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,853
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/AU93/00491
FILING DATE: 24-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PL 4973
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: BERT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/189/CHAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 280 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-403-853-10

Query Match 35.5%; Score 228; DB 1; Length 280;
Best Local Similarity 45.6%; Pred. No. 1.1e-17;
Matches 52; Conservative 20; Mismatches 36; Indels 6; Gaps 5;

QY 3 QRVSPDLRTWNLGRTVELKCOVLTLSNPTSGCSWLPQPRGA-AASPTFLYL--SONKPK 59
DB 28 ELRIFFPKMDAELGQKVDLVCEV-LGSVSGCSWLPQNSSKLPQPTFVVYMASSHNKIT 86
QY 60 AAEGLDTR-FSGKR-LGDTFVLTLSDFRRENGYFCSALNSIMYFSHFVPLV 111

Page 7

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 5, 2006, 15:51:00 ; Search time 51 Seconds

(without alignments)
1673.900 Million cell updates/sec

Title: US-09-560-494E-24

Perfect score: 642
Sequence: 1 MSQFVSPDLRTWNLGETVE.....IMYSPHFVPLPAKPTTTP 121

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: uniprot_05.80.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	637	99.2	235	1 CD8A_HUMAN	P01732 homo sapien
2	637	99.2	235	2 Q4ZG17_HUMAN	Q4ZG17 homo sapien
3	631	98.3	235	2 O96OR6_HUMAN	O96OR6 homo sapien
4	628	97.8	235	2 O8TAW8_HUMAN	O8TAW8 homo sapien
5	599	93.3	198	1 CD8A_PONPY	P04433 pongo pygma
6	547	85.2	235	2 O9XSM6_SAIISC	O9XSM6 salimiri sci
7	472	73.5	152	2 O6ZVW2_HUMAN	O6ZVW2 homo sapien
8	369.5	57.6	239	1 CD8A_CANPA	P33706 canis famli
9	366.5	57.1	239	1 CD8A_FELICA	P16688 felis silve
10	362	56.4	235	2 O6GRT4_PIG	O6GRT4 sus scrofa
11	347.5	54.1	242	1 CD8A_BOVIN	P1783 bos taurus
12	340	53.0	237	2 O6W8W8_CAVPO	O6W8W8 cavia porce
13	330	51.4	178	2 O6R4N4_PIG	O6R4N4 sus scrofa
14	330	51.4	195	2 O6R2U9_PIG	O6R2U9 sus scrofa
15	279.5	43.5	235	2 O8VH42_SIGHT	O8VH42 sigmodon hi
16	248	38.6	235	1 CD8A_RAT	P07725 rattus norv
17	239	37.2	222	2 O8CAK3_MOUSE	O8CAK3 mus musculu
18	239	37.2	240	1 CD8A_MOUSE	P01731 mus musculu
19	238	37.1	220	2 O61816_MOUSE	O61816 mus musculu
20	238	37.1	222	2 O8C2L1_MOUSE	O8C2L1 mus musculu
21	238	37.1	247	2 O60965_MOUSE	O60965 mus musculu
22	238	37.1	247	2 O542K6_MOUSE	O542K6 mus musculu
23	232	36.1	207	2 O8K2M2_MOUSE	O8K2M2 mus musculu
24	231	36.0	247	2 O8C2G0_MOUSE	O8C2G0 mus musculu
25	163.5	25.5	237	2 O50B04_CAIMO	O50B04 caimana mos
26	155	24.1	235	2 O90770_CHICK	O90770 gallus gall
27	154	24.0	235	2 O60R62_CHICK	O60R62 gallus gall
28	153	23.8	235	2 O60R65_CHICK	O60R65 gallus gall
29	153	23.8	235	2 O50E06_ANAPL	O50E06 anas platyr
30	152.5	23.8	237	2 O90W11_ANAPL	O90W11 anas platyr
31	151.5	23.6	2		

32	151	23.5	167	2 P79986_CHICK	P79986 gallus gall
33	151	23.5	235	2 O60R63_CHICK	O60R63 gallus gall
34	151	23.5	235	2 O60R64_CHICK	O60R64 gallus gall
35	147	22.9	235	2 O6R133_CHICK	O6R133 gallus gall
36	119.5	18.6	98	2 O5NV66_HUMAN	O5NV66 homo sapien
37	119	18.5	99	2 O5NV65_HUMAN	O5NV65 homo sapien
38	117.5	18.3	113	1 LV1_CHICK	P04210 gallus gall
39	117.5	18.3	266	2 O566X2_BRARE	O566X2 brachydanto
40	116.5	18.1	233	2 O6GWW4_HUMAN	O6GWW4 homo sapien
41	113.5	17.7	239	2 O6P491_HUMAN	O6P491 homo sapien
42	111.5	17.4	108	1 KV55_MOUSE	P01652 mus musculu
43	110	17.1	99	2 O5NV63_HUMAN	O5NV63 homo sapien
44	110	17.1	235	2 O6P583_HUMAN	O6P583 homo sapien
45	109.5	17.1	113	1 KV2G_MOUSE	P01631 mus musculu

ALIGNMENTS

RESULT 1	CD8A_HUMAN	STANDARD;	PRT;	235 AA.
AC	P01732; Q13970;			
DT	21-JUL-1986 (Ref. 01, Created)			
DT	21-JUL-1986 (Ref. 01, Last sequence update)			
DT	13-SEP-2005 (Ref. 48, Last annotation update)			
DE	T-cell surface glycoprotein CD8 alpha chain precursor (T-lymphocyte			
DE	differentiation antigen T8/Les-2).			
GN	Name=CD8A; Synonyms=ML;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE (ISOFORM 1).			
RX	MEDLINE=85099337; PubMed=3871356; DOI=10.1016/0092-8674(85)90138-2;			
RA	Littman D.R., Thomas Y., Madden P.U., Chess L., Axel R.;			
RT	"The isolation and sequence of the gene encoding T8: a molecule			
RT	defining functional classes of T lymphocytes."			
RL	Cell 40:237-246(1985).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE (ISOFORM 1).			
RX	MEDLINE=85124610; PubMed=3918796; DOI=10.1016/0092-8674(85)90207-7;			
RA	Sukhatme V.P., Sizer K.C., Volmer A.C., Hunkapiller T.;			
RT	"The T cell differentiation antigen Leu-2/T8 is homologous to			
RT	immunoglobulin and T cell receptor variable regions."			
RL	Cell 40:591-597(1985).			
RN	[4]			
RP	NUCLEOTIDE SEQUENCE (ISOFORM 2).			
RX	MEDLINE=90035142; PubMed=2509342;			
RA	Nakayama K.-I., Tokito S., Okumura K., Nakauchi H.;			
RT	"Structure and expression of the gene encoding CD8 alpha chain (Leu-			
RT	2/T8)."			
RL	Immunogenetics 30:393-397(1989).			
RN	[5]			
RP	NUCLEOTIDE SEQUENCE (ISOFORM 2), AND ALTERNATIVE SPLICING.			
RX	MEDLINE=92151302; PubMed=2491617;			
RA	Norment A.M., Lonberg N., Lacy E., Littman D.R.;			
RT	"Alternatively spliced mRNA encodes a secreted form of human CD8			
RT	alpha. Characterization of the human CD8 alpha gene."			
RL	J. Immunol. 142:3312-3319(1989).			
RN	[6]			
RP	NUCLEOTIDE SEQUENCE OF 168-235 (ISOFORMS 1 AND 2).			
RX	MEDLINE=89128905; PubMed=2536941;			
RA	Giblin P., Ledbetter J.A., Kavathas P.;			
RT	"A secreted form of the human lymphocyte cell surface molecule CD8			

RT arises from alternative splicing.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:998-1002(1989).
 RP [7]
 RA SUBUNIT.
 RX MEDLINE=84061928; PubMed=6605969;
 RT Snow P.M., Terhorst C.;
 RT "The T8 antigen is a multimeric complex of two distinct subunits on
 RT human thymocytes but consists of homomultimeric forms on peripheral
 RT blood T lymphocytes.";
 RL J. Biol. Chem. 258:14675-14681(1983).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 22-135.
 RX MEDLINE=92191292; PubMed=1547508; DOI=10.1016/0092-8674(92)90085-Q;
 RA Leahy D.J., Axel R., Hendrickson W.A.;
 RT "Crystal structure of a soluble form of the human T cell coreceptor
 RT CD8 at 2.6-A resolution.";
 RL Cell 68:1145-1162(1992).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS) OF 22-141 IN COMPLEX WITH
 RA HLA-B/B2M DIMER.
 RX MEDLINE=972320504; PubMed=9177355; DOI=10.1038/42523;
 RA Gao G.F., Formo J., Gerth U.C., Myer U.R., McMichael A.J.,
 RA Stuart D.I., Bell J.I., Jones E.Y., Jakobsen B.K.;
 RT "Crystal structure of the complex between human CD8alpha(alpha) and
 RT HLA-A2.";
 RL Nature 387:630-634(1997).
 RN [10]
 RP STRUCTURE BY NMR OF 209-227 IN COMPLEX WITH LCK.
 RX MEDLINE=22864827; PubMed=14500983; DOI=10.1126/science.1085643;
 RA Kim P.W., Sun Z.Y., Blacklow S.C., Wagner G., Eck M.J.;
 RT "A zinc clasp structure tethers Lck to T cell coreceptors CD4 and
 RT CD8.";
 RL Science 301:1725-1728(2003).
 RA [11]
 RP VARIANT CD8 DEFICIENCY SER-111, AND MUTAGENESIS OF GLY-111.
 RX MEDLINE=21329138; PubMed=11435463;
 RA de la Calle-Martin O., Hernandez M., Ordi J., Casanltjana N.,
 RA Arostegui J.I., Caragol I., Ferrando M., Labrador M.,
 RA Rodriguez-Sanchez J.L., Espanol T.,
 RT "Familial CD8 deficiency due to a mutation in the CD8 alpha gene.";
 RL J. Clin. Invest. 108:117-123(2001).
 CC -1- FUNCTION: Identifies cytotoxic/suppressor T-cells that interact
 CC with MHC class I bearing targets. CD8 is thought to play a role in
 CC the process of T-cell mediated killing. CD8 alpha chains binds to
 CC class I MHC molecules alpha-3 domains.
 CC -1- SUBUNIT: In general heterodimer of an alpha and a beta chain
 CC linked by two disulfide bonds. Can also form homodimers. Shown to
 CC be expressed as heterodimer on thymocytes and as homodimer on
 CC peripheral blood T lymphocytes. Interacts with the MHC class I
 CC HLA-A/B2M dimer. Interacts with LCK in a zinc-dependent manner.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1) and
 CC secreted (isoform 2).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=membrane, mCD8alpha;
 CC IsoId=P01732-1; Sequence=Displayed;
 CC Name=2; Synonyms=secreted, eCD8alpha;
 CC IsoId=P01732-2; Sequence=VSP_012653;
 CC -1- PTM: All of the five most carboxyl-terminal cysteines form inter-
 CC chain disulfide bonds in dimers and higher multimers, while the
 CC four N-terminal cysteines do not (By similarity).
 CC -1- DISEASE: Defects in CD8A are a cause of familial CD8 deficiency
 CC (CD8 deficiency) [MIM:608957]. Familial CD8 deficiency is a novel
 CC autosomal recessive immunologic defect characterized by absence of
 CC CD8+ cells, leading to recurrent bacterial infections.
 CC -1- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)
 CC domain.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC -----
 DR EMBL; M26315; AAA79217.1; -; Genomic_DNA.
 DR EMBL; M26313; AAA79217.1; JOINED; Genomic_DNA.
 DR EMBL; M26314; AAA79217.1; JOINED; Genomic_DNA.
 DR EMBL; M26315; AAA79218.1; -; Genomic_DNA.
 DR EMBL; M26313; AAA79218.1; JOINED; Genomic_DNA.
 DR EMBL; M26314; AAA79218.1; JOINED; Genomic_DNA.
 DR EMBL; M12824; AAA61133.1; -; mRNA.
 DR EMBL; M12828; AAB04637.1; -; mRNA.
 DR EMBL; M27161; AAB59674.1; -; Genomic_DNA.
 DR PIR; A30604; RWHUT8.
 DR PDB; 1AKJ; X-ray; D/B=22-141.
 DR PDB; 1CDJ; X-ray; @=-.
 DR PDB; 1Q69; NMR; A=209-227.
 DR Ensembl; ENSG00000153563; Homo sapiens.
 DR HGNC; HGNC:1706; CD8A.
 DR MIM; 186910; -.
 DR MIM; 608957; -.
 DR GO; GO:0005887; C:integral to plasma membrane; NAS.
 DR GO; GO:0042101; C:T cell receptor complex; NAS.
 DR GO; GO:0015026; F:coreceptor activity; NAS.
 DR GO; GO:0042288; F:MHC class I protein binding; NAS.
 DR GO; GO:0005515; F:protein binding; IPT.
 DR GO; GO:0019882; P:antigen presentation; NAS.
 DR GO; GO:0016066; P:cellular defense response (sensu Vertebrata); NAS.
 DR GO; GO:0042110; P:T cell activation; NAS.
 DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_V.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW 3D-structure; Alternative splicing; Disease mutation; Immune response;
 KW Immunoglobulin domain; Phosphorylation; Signal; T-cell; Transmembrane.
 FT SIGNAL 1 21
 FT CHAIN 1 21
 FT FT 22 235
 FT TOPO DOM 22 182
 FT TRANSMEM 183 203
 FT TOPO DOM 204 235
 FT DOMAIN 22 135
 FT DISULFID 43 115
 FT VARSPLIC 172 209
 FT FT 111 111
 FT VARIANT 111 111
 FT FT 111 111
 FT MOTAGEN 111 111
 FT STRAND 24 27
 FT TURN 35 36
 FT STRAND 39 45
 FT STRAND 45 59
 FT STRAND 54 59
 FT STRAND 68 73
 FT STRAND 79 80
 FT TURN 82 83
 FT TURN 86 88
 FT TURN 89 94
 FT STRAND 95 96
 FT TURN 97 102
 FT STRAND 107 109
 FT HELIX 107 119
 FT STRAND 111 119
 FT TURN 120 121
 FT TURN 120 125
 FT STRAND 122 125
 FT STRAND 129 131
 FT STRAND 129 131
 SQ SEQUENCE 235 AA; 25729 MW; FCCA29BA7726BB CRC64;
 Query Match 99.2%; Score 637; DB 1; Length 235;
 Best Local Similarity 100.0%; Pred. No. 9,9e-61;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2 SGRVSELDRTNWLGETVLEKCYVLLSNPTSGCSWLPQPGAAAPFFLLYLSQNKPKAA 61
 Db 22 SGRVSELDRTNWLGETVLEKCYVLLSNPTSGCSWLPQPGAAAPFFLLYLSQNKPKAA 81

Qy 62 EGLDTPRFGSKRLGDTFVLTLSDFRRENGEYFCSALNSIMYFSHFVPLPAKPTTP 121
 |||||||
 Db 82 EGLDTPRFGSKRLGDTFVLTLSDFRRENGEYFCSALNSIMYFSHFVPLPAKPTTP 141

RESULT 2

Q4ZG17_HUMAN
 ID Q4ZG17_HUMAN PRELIMINARY; PRT; 235 AA.
 AC Q4ZG17;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DE 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein CD8A.
 GN Name=CD8A;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Kruchowski S., Haakenson W., Boyer E.;
 RT "The sequence of Homo sapiens BAC clone RP11-81F3."
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Waterston R.H.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Waterston R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Wilson R.K.;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC064848; AX88864.1; -; Genomic_DNA.
 DR SMR; Q4ZG17; 22-135.
 DR Ensembl; ENSG00000153563; Homo sapiens.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Hypothetical protein; Immunoglobulin domain.
 KM Hypothetical protein; Immunoglobulin domain.
 SQ SEQUENCE 235 AA; 25729 MW; FCCA29BAA73726BB CRC64;

Query Match 99.2%; Score 637; DB 2; Length 235;
 Best Local Similarity 100.0%; Pred. No. 9.9e-61;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQFRVSPLDRTWNLGRTVELKCVLLSNPTSGCSWLPORGAASPTFLIYLSQNKPKAA 61
 |||||||
 Db 22 SQFRVSPLDRTWNLGRTVELKCVLLSNPTSGCSWLPORGAASPTFLIYLSQNKPKAA 81
 |||||||
 Qy 62 EGLDTPRFGSKRLGDTFVLTLSDFRRENGEYFCSALNSIMYFSHFVPLPAKPTTP 121
 |||||||
 Db 82 EGLDTPRFGSKRLGDTFVLTLSDFRRENGEYFCSALNSIMYFSHFVPLPAKPTTP 141

RESULT 3

Q96QR6_HUMAN
 ID Q96QR6_HUMAN PRELIMINARY; PRT; 235 AA.
 AC Q96QR6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mutant CD8 alpha antigen.
 GN Name=CD8A;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21329138; PubMed=11435463;
 RA de la Calle-Martin O., Hernandez M., Ordi J., Casamitjana N.,
 RA Arostegui J.I., Caragol I., Ferrando M., Labrador M.,
 RA Rodriguez-Sanchez J.L., Espanol T.;
 RT "Familial CD8 deficiency due to a mutation in the CD8 alpha gene."
 J. Clin. Invest. 108:117-123(2001).
 DR EMBL; AY039664; AA072403.1; -; mRNA.
 DR HSSP; P01732; 1CD8.
 DR SMR; Q96QR6; 22-135.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR SMART; SM00409; IG; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KM Immunoglobulin domain.
 SQ SEQUENCE 235 AA; 25759 MW; FCCA347AAEF732BB CRC64;

Query Match 98.3%; Score 631; DB 2; Length 235;
 Best Local Similarity 99.2%; Pred. No. 4.4e-60;
 Matches 119; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SQFRVSPLDRTWNLGRTVELKCVLLSNPTSGCSWLPORGAASPTFLIYLSQNKPKAA 61
 |||||||
 Db 22 SQFRVSPLDRTWNLGRTVELKCVLLSNPTSGCSWLPORGAASPTFLIYLSQNKPKAA 81
 |||||||
 Qy 62 EGLDTPRFGSKRLGDTFVLTLSDFRRENGEYFCSALNSIMYFSHFVPLPAKPTTP 121
 |||||||
 Db 82 EGLDTPRFGSKRLGDTFVLTLSDFRRENGEYFCSALNSIMYFSHFVPLPAKPTTP 141

RESULT 4

Q8TAW8_HUMAN
 ID Q8TAW8_HUMAN PRELIMINARY; PRT; 235 AA.
 AC Q8TAW8;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE CD8 antigen alpha polypeptide, isoform 1.
 GN Name=CD8A;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Pancreas;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stopleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.U., Ushed T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mollaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Maita M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

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RP NUCLEOTIDE SEQUENCE.
RC TISSUE=pancreas;
RA Struhsberg R.;
RL Submitted (Mar-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC025715; AAH25715.1; -, mRNA.
DR HSSP, P01732, 1CD8.
DR SMR, Q8TAW8, 22-135.
DR Ensembl, ENSG00000153563; Homo sapiens.
DR InterPro, IPR007110, Ig-like.
DR InterPro, IPR003596, Ig_v.
DR SMART, SM00406, IGV, 1.
DR PROSITE, PS50835, Ig_LIKE, 1.
KW Immunoglobulin domain.
SQ SEQUENCE 235 AA; 25669 MW; FCDPC9B5472D26BB CRC64;

Query Match
Best Local Similarity 97.8%; Score 628; DB 2; Length 235;
Matches 119; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SQFRVSPIDRTWNIGETVELKCOVLLSNPTSGCSWLFQPRGAASPTFLYLISQNKPKAA 61
DB 22 SQFRVSPIDRTWNIGETVELKCOVLLSNPTSGCSWLFQPRGAASPTFLYLISQNKPKAA 81
QY 62 EGLDQRFSGKRLGDTFVLTLSDFRRENGGYFCGALSNSIMYFSHFVVPFLPAKPTTP 121
DB 82 EGLDQRFSGKRLGDTFVLTLSDFRRENGGYFCGALSNSIMYFSHFVVPFLPAKPTTP 141

RESULT 5
CD8A_PONPY STANDARD; PRT; 198 AA.
AC P30433;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE T-cell surface glycoprotein CD8 alpha chain precursor (T-lymphocyte
DE differentiation antigen T8/Leu-2).
GN Name=CD8A;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Pongo.
OX NCBI_TaxId=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Isolate Jari;
RX MEDLINE=92307742; PubMed=1612644; DOI=10.1007/BF00215289;
RA Lawlor D.A., Farham P.;
RT "Structure of CD8 alpha and beta chains of the orangutan: novel
RT patterns of mRNA splicing encoding hingeless polypeptides.";
RL Immunogenetics 36:121-125 (1992).
CC -1- FUNCTION: Identifies cytotoxic/suppressor T-cells that interact
CC with MHC class I bearing targets. CD8 is thought to play a role in
CC the process of T-cell mediated killing. CD8 alpha chains binds to
CC class I MHC molecules alpha-3 domain.
CC -1- SUBUNIT: In general heterodimer of an alpha and a beta chain
CC linked by two disulfide bonds. Can also form homodimers.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)
CC domain.
CC -----
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL, X60223; CAA42784.1; -, mRNA.
DR PIR, S25656; S25656.
DR HSSP, P01732, 1CD8.
DR SMR, P30433; 22-134.
DR GO, GO:0042101, C: T cell receptor complex; ISS.
DR GO, GO:0015026, P: coreceptor activity; ISS.

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DR GO, GO:0042288, F: MHC class I protein binding; ISS.
DR GO, GO:0005515, F: protein binding; ISS.
DR GO, GO:0006955, P: immune response; ISS.
DR GO, GO:0042110, P: T cell activation; ISS.
DR GO, GO:0007169, P: transmembrane receptor protein tyrosine kin. ., ISS.
DR InterPro, IPR007110, Ig-like.
DR InterPro, IPR003596, Ig_v.
DR SMART, SM00406, IGV, 1.
DR PROSITE, PS50835, Ig_LIKE, 1.
KW Immune response; Immunoglobulin domain; Signal; T-cell; Transmembrane.
FT SIGNAL 1 21
FT CHAIN 22 198
FT TOPO DOM 22 145
FT TRANSMEM 146 166
FT TOPO DOM 167 198
FT DOMAIN 22 135
FT DISULFID 43 115
SQ SEQUENCE 198 AA; 22099 MW; F3EC093EADB05561 CRC64;

Query Match
Best Local Similarity 93.3%; Score 599; DB 1; Length 198;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQFRVSPIDRTWNIGETVELKCOVLLSNPTSGCSWLFQPRGAASPTFLYLISQNKPKAA 61
DB 22 SQFRVSPIDRTWNIGETVELKCOVLLSNPTSGCSWLFQPRGAASPTFLYLISQNKPKAA 81
QY 62 EGLDQRFSGKRLGDTFVLTLSDFRRENGGYFCGALSNSIMYFSHFVVPFL 114
DB 82 EGLDQRFSGKRLGDTFVLTLSDFRRENGGYFCGALSNSIMYFSHFVVPFL 134

RESULT 6
O9XSM6_SALSC
ID O9XSM6;
AC O9XSM6;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE CD8 alpha chain precursor.
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC Cebinae; Saimiri.
OX NCBI_TaxId=9521;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=92039;
RX MEDLINE=92399362; PubMed=10369934; DOI=10.1007/s002510050672;
RA Ureña-Vidal A., García Z., Lemmonier F.A., Kazanjli M.;
RT "Molecular characterization of cDNAs encoding squirrel monkey (saimiri
RT sciureus) CD8 alpha and beta chains.";
RL Immunogenetics 49:718-721 (1999).
DR EMBL, AJ130818; CAB41462.1; -, mRNA.
DR HSSP, P01732, 1CD8.
DR SMR, Q9XSM6; 22-135.
DR InterPro, IPR003599, Ig.
DR InterPro, IPR007110, Ig-like.
DR SMART, SM00409, IGV, 1.
DR PROSITE, PS50835, Ig_LIKE, 1.
KW Immunoglobulin domain; Signal.
FT SIGNAL 1 21
FT CHAIN 22 235
SQ SEQUENCE 235 AA; 25728 MW; 055867CD503C268D CRC64;

Query Match
Best Local Similarity 85.2%; Score 547; DB 2; Length 235;
Matches 99; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 2 SQFRVSPIDRTWNIGETVELKCOVLLSNPTSGCSWLFQPRGAASPTFLYLISQNKPKAA 61
DB 22 SQFRVSPIDRTWNIGETVELKCOVLLSNPTSGCSWLFQPRGAASPTFLYLISQNKPKAA 81

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QY 62 EGLDTPRSGKRLGDTFTLTSDPRFENEGYFCSALNSIMYFSHPVFLPAKPTTTP 121
 DB 82 DGLDAQRFSGKMGDSFTLTDRFREDQGFYFCSALNSIMYFSHPVFLPAKPTTTP 141
 RESULT 7
 06ZVS2 HUMAN
 ID 06ZVS2_HUMAN PRELIMINARY; PRT; 152 AA.
 AC 06ZVS2;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein FLJ42162.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Thymus;
 RA Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Sugiyama T.,
 RA Irie R., Otsubu T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
 RA Isono Y., Kawai-Hito Y., Saito K., Nishikawa T., Kimura K.,
 RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
 RA Magatsuna M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
 RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahara K.,
 RA Masuko Y., Nagai K., Isogai T.,
 RA Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK124156; BAC85789.1; -, mRNA.
 DR SMR; 06ZVS2; 63-152.
 SQ SEQUENCE 152 AA; 16713 MW; 6911F40F86122E02 CRC64;
 Query Match 73.5%; Score 472; DB 2; Length 152;
 Best local Similarity 100.0%; Pred. No. 5e-43; 0; Indels 0; Gaps 0;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 SQFRSPDLRTWNLGSETVLEKCVLLSNPTSGCSWLFQPRGAASPTFLYLSQNKPKA 61
 DB 63 SQFRSPDLRTWNLGSETVLEKCVLLSNPTSGCSWLFQPRGAASPTFLYLSQNKPKA 122
 QY 62 EGLDTPRSGKRLGDTFTLTSDPRFENEG 91
 DB 123 EGLDTPRSGKRLGDTFTLTSDPRFENEG 152
 RESULT 8
 CD8A_CANFA
 ID CD8A_CANFA STANDARD; PRT; 239 AA.
 AC P33706;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE T-cell surface glycoprotein CD8 alpha chain precursor.
 GN Name=CD8A;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 OC Canis.
 NCBI_TaxID=9615;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Beagle; TISSUE=Thymus;
 RX MEDLINE=94378217; PubMed=8091416;
 RA Gorman S.D., Frewin M.R., Cobbold S.P., Waldmann H.,
 RA "Isolation and expression of cDNA encoding the canine CD4 and CD8
 RT alpha antigens.",
 RT Tissue Antigens 43:184-188(1994).
 CC -1- FUNCTION: Identifies cytotoxic/suppressor T-cells that interact
 CC with MHC class I bearing targets. CD8 is thought to play a role in
 CC the process of T-cell mediated killing. CD8 alpha chains binds to
 CC class I MHC molecules alpha-3 domains.

CC -1- SUBUNIT: In general heterodimer of an alpha and a beta chain
 CC linked by two disulfide bonds. Can also form homodimers.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)
 CC domain.
 CC -----
 CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; L14287; AAB02294.1; -, mRNA.
 DR HSSP; P01732; 1CD8.
 DR Ensembl; ENSGAFG0000007464; Canis familiaris.
 DR GO; GO:0042101; C:T cell receptor complex; ISS.
 DR GO; GO:0015026; F:coreceptor activity; ISS.
 DR GO; GO:0042288; F:MHC class I protein binding; ISS.
 DR GO; GO:0005515; F:protein binding; ISS.
 DR GO; GO:0006955; P:immune response; ISS.
 DR GO; GO:0042110; P:T cell activation; ISS.
 DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; ISS.
 DR InterPro; IPR007110; Ig-like.
 DR SMART; SM00406; IG_V.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Glycoprotein; Immune response; Immunoglobulin domain; Signal; T-cell;
 KW Transmembrane.
 FT SIGNAL 1 21 Potential.
 FT CHAIN 22 239 T-cell surface glycoprotein CD8 alpha
 FT TOPO_DOM 22 186 chain.
 FT TRANSMEM 187 210 Extracellular (Potential).
 FT TOPO_DOM 211 239 Potential.
 FT DOMAIN 25 139 Cytoplasmic (Potential).
 FT CARBOHYD 156 156 Ig-like V-type.
 FT DISULFID 46 119 N-linked (GlcNAc. . .) (Potential).
 SQ SEQUENCE 239 AA; 26036 MW; 1018579779A5CB7B CRC64;
 Query Match 57.6%; Score 369.5; DB 1; Length 239;
 Best local Similarity 60.3%; Pred. No. 1.2e-31;
 Matches 73; Conservative 15; Mismatches 32; Indels 1; Gaps 1;
 QY 2 SQFRSPDLRTWNLGSETVLEKCVLLSNPTSGCSWLFQPRGAASPTFLYLSQNKPKA 61
 DB 25 SRRFMTPPRVQQLHAQVELQCQVLLSTAPGCSWLYQNEPAAAPVFLMYISQSRACKA 84
 QY 62 EGLDTPRSG-KRLGDTFTLTSDPRFENEGYFCSALNSIMYFSHPVFLPAKPTTTP 120
 DB 85 EGLDTPRSGKRLGDTFTLTSDPRFENEGYFCSALNSIMYFSHPVFLPAKPTTTP 144
 QY 121 P 121
 DB 145 P 145
 RESULT 9
 CD8A_FELCA
 ID CD8A_FELCA STANDARD; PRT; 239 AA.
 AC P41688;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE T-cell surface glycoprotein CD8 alpha chain precursor.
 GN Name=CD8A;
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
 OC Felinae; Felis.
 NCBI_TaxID=9685;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Thymus;

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RX MEDLINE=94176799; PubMed=8132208;
RA Pecora M., Kawaguchi Y., Miyazawa T., Norimine J., Maeda K.,
RA Toyosaki T., Tohya Y., Kai C., Mikami T.,
RT "Isolation, sequence and expression of a cDNA encoding the alpha-chain
RT of the feline CD8."
RL Immunology 81:127-131 (1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RA Miyazawa T.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Identifies cytotoxic/suppressor T-cells that interact
CC with MHC class I bearing targets. CD8 is thought to play a role in
CC the process of T-cell mediated killing. CD8 alpha chains binds to
CC class I MHC molecules alpha-3 domain.
CC -1- SUBUNIT: In general heterodimer of an alpha and a beta chain
CC linked by two disulfide bonds. Can also form homodimers.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. (immunoglobulin-like)
CC domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: D16536; BAA03973.1; -; mRNA.
CC EMBL: AB000485; BAA19126.1; -; mRNA.
CC PIR: I46082; I46082.
CC HSPD: P01732; 1CD8.
CC DR GO: GO:0042101; C: T cell receptor complex; ISS.
CC DR GO: GO:0015026; F: coreceptor activity; ISS.
CC DR GO: GO:0042288; F: MHC class I protein binding; ISS.
CC DR GO: GO:0005515; F: protein binding; ISS.
CC DR GO: GO:0006955; P: immune response; ISS.
CC DR GO: GO:0042110; P: T cell activation; ISS.
CC DR GO: GO:007169; P: transmembrane receptor protein tyrosine kin. .; ISS.
CC DR InterPro: IPR003599; IG.
CC DR InterPro: IPR007110; IG-like.
CC DR Pfam: PF00047; IG_1.
CC DR SMART: SM00409; IG; 1.
CC DR PROSITE: PS50835; IG_LIKE; 1.
CC KM Immune response; immunoglobulin domain; signal; T-cell; Transmembrane.
CC FT SIGNAL 1 21 Potential.
CC FT CHAIN 22 239 T-cell surface glycoprotein CD8 alpha chain.
CC FT TOPO_DOM 22 188 Extracellular (Potential).
CC FT TRANSMEM 189 210 Potential.
CC FT TOPO_DOM 211 239 Cytoplasmic (Potential).
CC FT DOMAIN 25 139 Ig-like V-type.
CC FT DISULFID 46 119 By similarity.
CC SQ SEQUENCE 239 AA; 26120 MW; F9A171820B8FF1BC CRC64;

Query Match 57.1%; Score 366.5; DB 1; Length 239;
Best Local Similarity 58.7%; Pred. No. 2.5e-31;
Matches 71; Conservative 19; Mismatches 30; Indels 1; Gaps 1;

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ID O6GYR4_PIG PRELIMINARY; PRT; 236 AA.
AC O6GYR4;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE CD8 antigen alpha protein.
OS Sus scrofa (pig).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;
OC Sus.
OC NCBI_TaxId=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wang J., Yang H., Guo X.;
RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY590798; AAT52341.1; -; mRNA.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-LIKE.
DR InterPro: IPR003596; IG_V.
DR SMART: SM00409; IG; 1.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KM Immunoglobulin domain.
SQ SEQUENCE 236 AA; 26329 MW; FFE3887B155B7EC CRC64;

Query Match 56.4%; Score 362; DB 2; Length 236;
Best Local Similarity 57.5%; Pred. No. 7.5e-31;
Matches 69; Conservative 19; Mismatches 32; Indels 0; Gaps 0;

OY 2 S0FRVSPIDRTWNLGETVELKCOVLLSNPTSGCSWLFQPRGAASPTFLYLTSQNKPKAA 61
DB 25 SUFFRSPENWASLGEIVLQCEVLLSSAAPGCTWLFQKNEPAARIFLAFLYSRSTKA 84
OY 62 EBLDTRFSGKRLGDT-FVLLTSDPRENEGYYFCGALSNSIMYFSHPVPLPAKPTTP 121
DB 85 EBLDTRFISGVKXANDNPLILHRFREDQGYFFCGFLNSVLFENFMSVFLPAKPTKP 144

RESULT 11
CD8A_BOVIN STANDARD; PRT; 242 AA.
ID CD8A_BOVIN
AC P31783;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE T-cell surface glycoprotein CD8 alpha chain precursor.
GN Name=CD8A;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OC NCBI_TaxId=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RA MEDLINE=92332098; PubMed=1628904;
RA Lalor P., Buccì C., Fornaro M., Rattazzi M.C., Nakaguchi H.,
RA Herzenberg L.A., Alberti S.;
RT "Molecular cloning, reconstruction and expression of the gene encoding
RT the alpha-chain of the bovine CD8 -- definition of three peptide
RT regions conserved across species.";
RL Immunology 76:95-102 (1992).
CC -1- FUNCTION: Identifies cytotoxic/suppressor T-cells that interact
CC with MHC class I bearing targets. CD8 is thought to play a role in
CC the process of T-cell mediated killing. CD8 alpha chains binds to
CC class I MHC molecules alpha-3 domain.
CC -1- SUBUNIT: In general heterodimer of an alpha and a beta chain
CC linked by two disulfide bonds. Can also form homodimers.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)
CC domain.
CC -----
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CC removed.

DR EMBL: X59416; CAA42051.1; -, mRNA.
DR PIR: S25663; S25663.
DR HSSP: P01732; 1CD8.
DR GO: GO:0042101; C.T cell receptor complex; ISS.
DR GO: GO:0015026; F:coreceptor activity; ISS.
DR GO: GO:0042288; F:MHC class I protein binding; ISS.
DR GO: GO:0005515; F:protein binding; ISS.
DR GO: GO:0006955; P:immune response; ISS.
DR GO: GO:0042110; P:T cell activation; ISS.
DR GO: GO:0007169; P:transmembrane receptor protein tyrosine kin. .; ISS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immune response; Immunoglobulin domain; Signal; T-cell; Transmembrane.
FT SIGNAL 1 25
FT CHAIN 26 242
FT 26 242
FT TOPO DOM 26 189
FT TRANSMEM 190 214
FT TOPO DOM 215 242
FT DOMAIN 26 140
FT DISULFID 47 120
SQ SEQUENCE 242 AA; 26417 MW; 91481320EP05195E CRC64;

Query Match
Best Local Similarity 54.1%; Score 347.5; DB 1; Length 242;
Matches 68; Conservative 17; Mismatches 33; Indels 1; Gaps 1;

Qy 4 FVSPVPLDRTNWIGETVELKCOVLINPTSGCSWLFQPRGAASPTFLYLSQNKPKAEG 63
Db 28 FVSPVPLDRTNWIGETVELKCOVLINPTSGCSWLFQPRGAASPTFLYLSQNKPKAEG 63
64 LDTORFSGKRL-GDPFVLTLSDFRRENGGYFCSALNSIMVFSHFVPLPAKPTTTP 121
88 LDPRIHISGAKVSGTKFQLTSLSPLODQGYFCVSIVNSILYFSNFPVFLPAKPTTTP 146

RESULT 12
O6M8W8_CAVPO PRELIMINARY; PRT; 237 AA.

AC O6M8W8; 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CD8 alpha.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed:14705950; DOI=10.1111/j.1399-0039.2004.00155.x;
RA Nagai et al. U.M., O'Connell C., Rank R.G.;
RT "Molecular characterization of guinea - pig (Cavia porcellus) CD8alpha
RT and CD8beta cDNA."
RL Tissue Antigens 63:184-189(2004).
DR EMBL: AY03773; AA073501.1; -, mRNA.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR SMART: SM00409; IGV; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 237 AA; 25627 MW; 5358FAD87D6A9B6 CRC64;

Query Match
Best Local Similarity 53.0%; Score 340; DB 2; Length 237;
Matches 64; Conservative 20; Mismatches 36; Indels 0; Gaps 0;

Qy 2 SGRVSPVPLDRTNWIGETVELKCOVLINPTSGCSWLFQPRGAASPTFLYLSQNKPKA 61
Db 27 SGRVSPVPLDRTNWIGETVELKCOVLINPTSGCSWLFQPRGAASPTFLYLSQNKPKA 61
62 EGIIDTQRFSGKRLGDTFVLTLSDFRRENGGYFCSALNSIMVFSHFVPLPAKPTTTP 121
87 PGLGQRFPSPKSSNTYLTIVNSFQKRDGYFCVSIVNSILYFSNFPVFLPAKPTTTP 146

RESULT 13
O6R4N4_PIG PRELIMINARY; PRT; 178 AA.

AC O6R4N4; 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CD8 antigen alpha polypeptide (Fragment).
GN Name=CD8A;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wang J., Yang H., Guo X.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY514489; AAR98817.1; -, mRNA.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1 178
SQ SEQUENCE 178 AA; 20160 MW; AD373258B32D9BB1 CRC64;

Query Match
Best Local Similarity 51.4%; Score 330; DB 2; Length 178;
Matches 60; Conservative 18; Mismatches 25; Indels 0; Gaps 0;

Qy 19 VELKQVLINPTSGCSWLFQPRGAASPTFLYLSQNKPKAEGIDTQRFSGKRLGDTF 78
Db 1 VELKQVLINPTSGCSWLFQPRGAASPTFLYLSQNKPKAEGIDTQRFSGKRLGDTF 78
79 VLTLSDFRRENGGYFCSALNSIMVFSHFVPLPAKPTTTP 121
61 VLTLSDFRRENGGYFCSALNSIMVFSHFVPLPAKPTTTP 103

RESULT 14
O6R2U9_PIG PRELIMINARY; PRT; 195 AA.

AC O6R2U9; 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CD8 antigen alpha protein (Fragment).
GN Name=CD8A;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wang J., Yang H., Guo X.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY517855; AAS01522.1; -, mRNA.
DR InterPro: IPR007110; Ig-like.

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 5, 2006, 15:50:39 ; Search time 81 Seconds
(without alignments)
656.356 Million cell updates/sec

Title: US-09-560-494E-24

Perfect score: 642

Sequence: 1 MSQFRVSPIDRTWNLGETVE.....IMYFSHFVFLPAKPTTP 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_21.*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	642	100.0	121	2	AAV21689
2	637	99.2	198	8	AD92792
3	637	99.2	198	8	AD92792
4	637	99.2	198	8	AD92792
5	637	99.2	198	8	AD92792
6	637	99.2	198	8	AD92792
7	637	99.2	198	8	AD92792
8	637	99.2	198	8	AD92792
9	637	99.2	198	8	AD92792
10	637	99.2	198	8	AD92792
11	637	99.2	198	8	AD92792
12	637	99.2	198	8	AD92792
13	637	99.2	198	8	AD92792
14	637	99.2	198	8	AD92792
15	637	99.2	198	8	AD92792
16	637	99.2	198	8	AD92792
17	637	99.2	198	8	AD92792
18	637	99.2	198	8	AD92792
19	637	99.2	198	8	AD92792
20	637	99.2	198	8	AD92792
21	637	99.2	198	8	AD92792
22	637	99.2	198	8	AD92792
23	637	99.2	198	8	AD92792
24	637	99.2	198	8	AD92792

25	547	85.2	235	8	AD92814	Ad92814 Amino aci
26	547	85.2	235	8	AD92814	Ad92814 Common sq
27	472	73.5	152	8	AD92810	Ad92810 Novel hum
28	366.5	57.1	239	8	AD92810	Ad92810 Amino aci
29	366.5	57.1	239	8	AD92810	Ad92810 Cat CD8 a
30	347.5	54.1	242	8	AD92806	Ad92806 Amino aci
31	347.5	54.1	242	8	AD92806	Ad92806 Cow CD8 a
32	340	53.0	237	8	AD92804	Ad92804 Amino aci
33	340	53.0	237	8	AD92804	Ad92804 Guinea pi
34	330	51.4	195	8	AD92808	Ad92808 Amino aci
35	330	51.4	195	8	AD92808	Ad92808 Domestic
36	279.5	43.5	235	8	AD92812	Ad92812 Amino aci
37	279.5	43.5	235	8	AD92812	Ad92812 H1spid co
38	248	38.6	236	8	AD92802	Ad92802 Amino aci
39	248	38.6	236	8	AD92802	Ad92802 Rat CD8 a
40	239	37.2	130	2	AAV21691	AAV21691 Expressed
41	239	37.2	247	2	AAV21690	AAV21690 Mouse CD8
42	239	37.2	282	2	AAV21690	AAV21690 Sequence
43	239	37.2	310	8	AD92818	Ad92818 Amino aci
44	239	37.2	310	8	AD92796	Ad92796 Amino aci
45	239	37.2	310	8	AD92796	Ad92796 Murine CD

ALIGNMENTS

RESULT 1	AAV21689	standard; protein; 121 AA.
ID	AAV21689	standard; protein; 121 AA.
AC	AAV21689;	
XX		
DT	18-AUG-1999	(first entry)
DE	Expressed fragment of human CD8 alpha protein.	
KM	T lymphocyte inhibition; CD8; immunosuppressive therapy; transplantation;	
KW	autoimmune disease; allergy; asthma; viral infection; cytotoxic;	
KM	corticosteroid; human; CD8 alpha protein.	
XX		
OS	Homo sapiens.	
XX		
PN	WO921576-A1.	
XX		
PD	06-MAY-1999.	
XX		
PF	28-OCT-1998;	98WO-GB003235.
XX		
PR	28-OCT-1997;	97GB-00022779.
XX		
PA	(ISIS-) ISIS INNOVATION LTD.	
PI	Jakobsen BK, Gao GF, Gerth UC, Sewell AK;	
DR	WPI; 1999-385058/32.	
XX	N-PSDB; AAX80968.	
PT	Inhibiting activity of T cells against target cells useful for treating	
PT	autoimmune diseases and allergy.	
XX		
PS	Claim 9; Fig 1B; 79p; English.	
CC	The invention describes a method for inhibiting activity of T lymphocytes	
CC	against a target cell by treating the cell with a soluble form of a CD8	
CC	molecule. The method is used as immunosuppressive therapy, e.g. in	
CC	patients undergoing transplantation, but also for treating autoimmune	
CC	diseases and allergy, e.g. exacerbation of asthma caused by viral	
CC	infection. The CD8 protein inhibits cytotoxic T cells in vitro or in	
CC	vivo, and its inhibitory activity can be adjusted by mutation. Treatment	
CC	with CD8 protein provides more selective immunosuppression than use of	
CC	corticosteroids. The present sequence represents the expressed fragment	
CC	of human CD8 alpha protein	
XX		

SQ Sequence 121 AA;

Query Match 100.0%; Score 642; DB 2; Length 121;
 Best Local Similarity 100.0%; Pred. No. 1.3e-63;
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQFVSPIDRTWNGETVELKCOVLLSNPTSGCSWLFPPRGAAASPTFLVLSQNKPKXA 60
 |||
 DB 1 MSQFVSPIDRTWNGETVELKCOVLLSNPTSGCSWLFPPRGAAASPTFLVLSQNKPKXA 60
 |||

QY 61 AEGLDTORFSGKRLGDTFVLTLSDFRRENEGYYFCGALSNSIMYFSHFVPLPAKPTTT 120
 |||
 DB 61 AEGLDTORFSGKRLGDTFVLTLSDFRRENEGYYFCGALSNSIMYFSHFVPLPAKPTTT 120
 |||

QY 121 P 121
 |||
 DB 121 P 121
 |||

RESULT 2
 ADS92792
 ID ADS92792 standard; protein; 198 AA.
 XX
 AC ADS92792;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE A secreted CD8 alpha-chain protein alternative transcript.
 XX
 KW immune response; cell-specific antigen; alloantigen; CD8;
 KM CD8 alpha-chain; cellular immune response; humoral immune response;
 XX transplant allograft; graft-versus-host disease; transplant.
 OS Homo sapiens.
 XX
 PN WO2004083244-A2.
 XX
 PD 30-SEP-2004.
 XX
 PE 19-MAR-2004; 2004WO-US008574.
 XX
 PR 19-MAR-2003; 2003US-0456378P.
 XX
 PA (ISOG-) ISOGENTIS INC.
 XX
 PI Qi Y, Zhang X, Konigsberg PJ;
 XX
 DR WPI; 2004-691022/67.
 DR N-PSDB; ADS92793.
 XX

PS Disclosure; Fig 1; 98pp; English.

XX The specification describes a method for specifically inhibiting a host
 CC immune response to target cell-specific antigens (e.g. alloantigens). The
 CC method comprises contacting a target cell expressing the antigen with an
 CC expression vector encoding a CD8 polypeptide comprising the CD8 alpha-
 CC chain, where the CD8 polypeptide is expressed by the target cell and
 CC where the host immune response against the target cell is specifically
 CC inhibited. The method of the invention is useful for specifically
 CC inhibiting both cellular and humoral immune responses to alloantigens,
 CC thus finding use in extending the survival of transplant allografts and
 CC in treating graft-versus-host disease in transplant recipients. The
 CC present sequence represents an alternative transcript of a secreted alpha
 CC chain of a CD8 protein. This CD8 alpha-chain may be used in the method
 CC of the invention.
 XX
 SQ Sequence 198 AA;

Query Match 99.2%; Score 637; DB 8; Length 198;
 Best Local Similarity 100.0%; Pred. No. 9e-63;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQFVSPIDRTWNGETVELKCOVLLSNPTSGCSWLFPPRGAAASPTFLVLSQNKPKXA 61
 |||
 DB 22 SQFVSPIDRTWNGETVELKCOVLLSNPTSGCSWLFPPRGAAASPTFLVLSQNKPKXA 81
 |||

QY 62 EGLDQRFSGKRLGDTFVLTLSDFRRENEGYYFCGALSNSIMYFSHFVPLPAKPTTT 121
 |||
 DB 62 EGLDQRFSGKRLGDTFVLTLSDFRRENEGYYFCGALSNSIMYFSHFVPLPAKPTTT 141
 |||

RESULT 3
 ADS19438
 ID ADS19438 standard; protein; 198 AA.
 XX
 AC ADS19438;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Human secreted protein related to the CD8 alpha chain protein.
 XX
 KW human; gene therapy; CD8 alpha chain; cellular immune response;
 KM humoral immune response; immunosuppressive.
 XX
 OS Homo sapiens.
 XX
 PN WO2004083404-A2.
 XX
 PD 30-SEP-2004.
 XX
 PE 19-MAR-2004; 2004WO-US008567.
 XX
 PR 19-MAR-2003; 2003US-0456378P.
 XX
 PA (ISOG-) ISOGENTIS INC.
 XX
 PI Qi Y, Zhang X, Konigsberg PJ;
 XX
 DR WPI; 2004-691049/67.
 DR N-PSDB; ADS19439.
 XX

PS Disclosure; Fig 1; 94pp; English.

XX This invention relates to novel gene therapy vectors with reduced
 CC immunogenicity. Specifically, it refers to a nucleic acid encoding a CD8
 CC alpha chain operably linked to nucleic acid encoding a transmembrane
 CC polypeptide and a second nucleic acid representing the therapeutic gene
 CC of interest (for example oncolytic cardamoyl transferase or beta
 CC glucosidase), whereby transcriptional and translational control elements
 CC direct expression thereof. The present invention describes a method to
 CC reduce an immune response against antigens derived from a gene therapy
 CC delivery system i.e. improving the expression of a therapeutic transgene
 CC in a host and improving viral expression vectors with reduced
 CC immunogenicity. Accordingly, these compositions are useful for inhibiting
 CC both the cellular and humoral components of the host immune responses
 CC against expression vectors and target cells transfected with the vectors.
 CC As such, they exhibit immunosuppressive activity. This polypeptide is a
 CC human secreted protein related to the CD8 alpha chain protein of the
 CC invention.
 XX
 SQ Sequence 198 AA;

Query Match 99.2%; Score 637; DB 8; Length 198;
 Best Local Similarity 100.0%; Pred. No. 9e-63;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQFRVSPDLRTWNLGRTVELKQVLLSNPTSGCSWLFQPRGAASPTFLLYLSQNKPKAA 61
 DB 22 SQFRVSPDLRTWNLGRTVELKQVLLSNPTSGCSWLFQPRGAASPTFLLYLSQNKPKAA 81
 QY 62 EGLDTRFSGKRLGDTFVLTLSDFRRENGYFCSALSNIMYFSHVVPVFLPAKPTTTP 121
 DB 82 EGLDTRFSGKRLGDTFVLTLSDFRRENGYFCSALSNIMYFSHVVPVFLPAKPTTTP 141

RESULT 4

ID ADZ26404 standard; protein; 198 AA.

ADZ26404;

16-JUN-2005 (first entry)

Human CD8.

cell culture; stem cell; CD8.

Homo sapiens.

MO2005030999-A1.

07-APR-2005.

24-SEP-2004; 2004MO-US031524.

25-SEP-2003; 2003US-0506221P.

08-OCT-2003; 2003US-0509594P.

(DAND) DANA FARBER CANCER INST INC.

Ritz J, Wu CJ;

WPI; 2005-273394/28.

N-PSDB; ADZ26403.

detecting lineage-specific cells in a biological sample, useful for

disclosure; SEQ ID NO 30; 393bp; English.

The invention relates to a method of detecting lineage-specific cells in a biological sample which comprises identifying lineage-specific mRNA in the sample. The methods are useful for determining the clinical outcome of a progenitor cell transfer in a subject, and for identifying or quantifying lineage-specific cells. The present sequence represents the amino acid sequence of a human protein used to identify lineage-specific cells.

Sequence 198 AA;

Query Match 99.2%; Score 637; DB 9; Length 198;

Best Local Similarity 100.0%; Pred. No. 9e-63;

Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQFRVSPDLRTWNLGRTVELKQVLLSNPTSGCSWLFQPRGAASPTFLLYLSQNKPKAA 61

DB 22 SQFRVSPDLRTWNLGRTVELKQVLLSNPTSGCSWLFQPRGAASPTFLLYLSQNKPKAA 81

QY 62 EGLDTRFSGKRLGDTFVLTLSDFRRENGYFCSALSNIMYFSHVVPVFLPAKPTTTP 121

DB 82 EGLDTRFSGKRLGDTFVLTLSDFRRENGYFCSALSNIMYFSHVVPVFLPAKPTTTP 141

RESULT 5

AAR49550 standard; protein; 235 AA.

AAR49550;

XX 25-MAR-2003 (revised)

XX 20-AUG-1994 (first entry)

XX Sequence of human CD8.

XX gp39; T-cell antigen; CD40 ligand; B-cell proliferation; CD8;

XX fusion protein; CD8; fusion protein.

XX Homo sapiens.

XX EP585943-A2.

XX 09-MAR-1994.

XX 03-SEP-1993; 93EP-00114153.

XX 04-SEP-1992; 92US-00940605.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Aruffo A, Hollenbaugh D, Ledbetter JA;

XX WPI; 1994-076264/10.

XX N-PSDB; AAQ57986.

XX New nucleic acid encoding human gp39 T cell antigen - which is a ligand

XX for the CD40 receptor, causing proliferation and differentiation of B

XX cells and some cancer cells.

XX Disclosure; Fig 9; 39pp; English.

The complete nucleic acid sequence of human gp39 (hgp39) protein (corresp. to cDNA) and the complete AA sequence of hgp39 are presented in AAQ57984 and AAR49548 respectively and contd. in plasmid CDW8-hgp39, deposited with the ATCC as E. coli, CDW8 MC1061/p3-hgp39 and assigned accession No. 69050. The human T cell antigen gp39 is a ligand for the CD40 receptor. Soluble gp39 may be produced using the expression vector CC CD8-gp39. Chimeric genes may be constructed by fusing sequences encoding the extracellular domains of gp39 and CD8, pref. murine or human CD8 protein. Plasmid p3-hgp39 encoding the fusion protein of the extracellular domains from gp39 and CD8 is deposited in E. coli as ATCC 69049. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 235 AA;

Query Match 99.2%; Score 637; DB 2; Length 235;

Best Local Similarity 100.0%; Pred. No. 1.1e-62;

Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQFRVSPDLRTWNLGRTVELKQVLLSNPTSGCSWLFQPRGAASPTFLLYLSQNKPKAA 61

DB 22 SQFRVSPDLRTWNLGRTVELKQVLLSNPTSGCSWLFQPRGAASPTFLLYLSQNKPKAA 81

QY 62 EGLDTRFSGKRLGDTFVLTLSDFRRENGYFCSALSNIMYFSHVVPVFLPAKPTTTP 121

DB 82 EGLDTRFSGKRLGDTFVLTLSDFRRENGYFCSALSNIMYFSHVVPVFLPAKPTTTP 141

RESULT 6

AAZ21688 standard; protein; 235 AA.

AAZ21688;

18-AUG-1999 (first entry)

Human CD8 alpha protein.

T lymphocyte inhibition; CD8; immunosuppressive therapy; transplantation; autoimmune disease; allergy; asthma; viral infection; cytotoxic;

corticosteroid; human; CD8 alpha protein.

OS Homo sapiens.
 XX WO9921576-A1.
 XX 06-MAY-1999.
 XX
 XX 28-OCT-1998; 98WO-GB003235.
 XX
 XX 28-OCT-1997; 97GB-00022779.
 XX
 XX (ISIS-) ISIS INNOVATION LTD.
 XX
 XX Jakobsen BK, Gao GF, Gerth UC, Sewell AK;
 XX WPI, 1999-385058/32.
 XX N-PSDB; AAX80967.
 XX
 XX Inhibiting activity of T cells against target cells useful for treating
 XX autoimmune diseases and allergy.
 XX
 XX Disclosure; Fig 1A; 79pp; English.
 XX
 XX The invention describes a method for inhibiting activity of T lymphocytes
 XX against a target cell by treating the cell with a soluble form of a CD8
 XX molecule. The method is used as immunosuppressive therapy, e.g. in
 XX patients undergoing transplantation, but also for treating autoimmune
 XX diseases and allergy, e.g. exacerbation of asthma caused by viral
 XX infection. The CD8 protein inhibits cytotoxic T cells in vitro or in
 XX vivo, and its inhibitory activity can be adjusted by mutation. Treatment
 XX with CD8 protein provides more selective immunosuppression than use of
 XX corticosteroids. The present sequence represents a human CD8 alpha
 XX protein
 XX
 XX Sequence 235 AA;
 XX
 XX
 XX Query Match 99.2%; Score 637; DB 2; Length 235;
 XX Best Local Similarity 100.0%; Pred. No. 1.1e-62;
 XX Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 2 SQFRVSPLDRTWNLGRTVELKCOVLLSNPTSGCSWLFOPRGAASPTFLYLISQNKPKAA 61
 XX |||||||
 XX 22 SQFRVSPLDRTWNLGRTVELKCOVLLSNPTSGCSWLFOPRGAASPTFLYLISQNKPKAA 81
 XX |||||||
 XX QY 62 EGLDTRFSGKRLGDTFVLTLSDFRRENGGYFCALSNSIMYFSHFVPLPAKPTTP 121
 XX |||||||
 XX DB 82 EGLDTRFSGKRLGDTFVLTLSDFRRENGGYFCALSNSIMYFSHFVPLPAKPTTP 141
 XX |||||||
 XX
 XX RESULT 7
 XX ABP54792
 XX ID ABP54792 standard; protein; 235 AA.
 XX
 XX AC ABP54792;
 XX
 XX 30-DEC-2002 (first entry)
 XX
 XX Human CD8.
 XX
 XX Chronic obstructive pulmonary disease; COPD; antagonist; CD8; human;
 XX transgenic animal; transgenic plant; antiasthmatic; antiinflammacy;
 XX antiarthritic; osteopathic; dermatological; immunosuppressive; cardiac;
 XX antiarteriosclerotic; hypotensive; antianginal; antibacterial; virucide;
 XX fungicide; parasiticide; cytostatic; nootropic; neuroprotective;
 XX antiparkinsonian; gene therapy.
 XX
 XX Homo sapiens.
 XX
 XX OS
 XX
 XX Key Location/Qualifiers
 XX Region 22..118
 XX /note= "epitope bound by COPD-related Ig-derived protein"
 XX FT 119..235
 XX /note= "epitope bound by COPD-related Ig-derived protein"
 XX FT
 XX

PN WO200272788-A2.
 XX
 XX 19-SEP-2002.
 XX
 XX 14-MAR-2002; 2002WO-US007946.
 XX
 XX 14-MAR-2001; 2001US-0275652P.
 XX
 XX (CENZ) CENTOCOR INC.
 XX
 XX Torphy T;
 XX WPI, 2002-740810/80.
 XX
 XX New isolated chronic obstructive pulmonary disease (COPD) related
 XX immunoglobulin derived protein or variant, useful for treating COPD-
 XX related conditions such as emphysema, asthma, chronic bronchitis or
 XX airflow obstruction.
 XX
 XX Claim 2; Page 108-109; 126pp; English.
 XX
 XX The present sequence is that of human CD8, an example of a chronic
 XX obstructive pulmonary disease (COPD)-related protein. The invention
 XX relates to novel COPD-related immunoglobulin (Ig)-derived proteins (see
 XX ABP54799-803) comprising at least one Ig complementarily determining
 XX region or at least one ligand binding region that specifically binds to
 XX at least one COPD-related protein, e.g. binding at least 1-3 amino acids,
 XX to the entire sequence, of amino acids 22-118 and 119-235 of the present
 XX sequence. The human COPD-related Ig-derived proteins act as antagonists
 XX to the COPD-related proteins. The invention provides the COPD-related Ig-
 XX encoded proteins or specified portions or variants of them, nucleic acids
 XX encoding these polypeptides, vectors, host cells, transgenic animals and
 XX transgenic plants, and methods of making the COPD-related Ig-derived
 XX proteins, including therapeutic compositions. The proteins, nucleic
 XX acids, formulations and compositions are useful for treating COPD-related
 XX conditions such as COPD, emphysema, asthma, chronic bronchitis or airflow
 XX obstruction (claimed). They are also useful for treating or modulating
 XX COPD associated immune related diseases (arthritis, osteoarthritis,
 XX allergic rhinitis, lupus), cardiovascular diseases (congestive heart
 XX failure, arteriosclerosis, hypertension, angina pectoris), infections
 XX (bacterial, viral, fungal, parasitic), malignant diseases (cancer,
 XX leukaemia, Hodgkin's disease) and/or neurological diseases (Huntington's
 XX disease, Parkinson's disease, multiple sclerosis)
 XX
 XX Sequence 235 AA;
 XX
 XX
 XX Query Match 99.2%; Score 637; DB 5; Length 235;
 XX Best Local Similarity 100.0%; Pred. No. 1.1e-62;
 XX Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 2 SQFRVSPLDRTWNLGRTVELKCOVLLSNPTSGCSWLFOPRGAASPTFLYLISQNKPKAA 61
 XX |||||||
 XX DB 22 SQFRVSPLDRTWNLGRTVELKCOVLLSNPTSGCSWLFOPRGAASPTFLYLISQNKPKAA 81
 XX |||||||
 XX QY 62 EGLDTRFSGKRLGDTFVLTLSDFRRENGGYFCALSNSIMYFSHFVPLPAKPTTP 121
 XX |||||||
 XX DB 82 EGLDTRFSGKRLGDTFVLTLSDFRRENGGYFCALSNSIMYFSHFVPLPAKPTTP 141
 XX |||||||
 XX
 XX RESULT 8
 XX AAO19807
 XX ID AAO19807 standard; protein; 235 AA.
 XX
 XX AC AAO19807;
 XX
 XX 11-AUG-2003 (first entry)
 XX
 XX Human CD8alpha chain protein.
 XX
 XX Human; CD8alpha; MHC binding; mutant; mutein; immunosuppressive;
 XX antiallergic; cytotoxic T cell response; inhibitor.
 XX
 XX Homo sapiens.
 XX
 XX OS

XX MO2002102852-A2.
PN 27-DEC-2002.
XX
PD 14-JUN-2002; 2002WO-GB002743.
XX
PR 14-JUN-2001; 2001GB-00014533.
XX
PA (AVID-) AVIDEX LTD.
XX
PI Jakobsen BK, Glick M;
XX WPI; 2003-167488/16.
DR N-PSDB; AB269260.
XX
PT New modified CD8 molecule having enhanced binding to major
PT histocompatibility complex, and having a Serine53 of at least one CD
PT alpha chain is mutated to another amino acid, useful for treating e.g.
PT graft rejection or hypersensitivity.
XX
PS Disclosure; Fig 1A; 60pp; English.
XX
CC The present invention provides modified human CD8 molecules whose binding
CC to major histocompatibility complex (MHC) is enhanced compared to wild
CC type CD8. The modified CD8 molecule or a corresponding nucleic acid is
CC useful in medicine, particularly in manufacturing a medicament for
CC modulating CD8+ T cell response. The modified CD8 proteins and nucleic
CC acids encoding such proteins are useful in immunosuppressive therapy,
CC particularly as inhibitors of cytotoxic T cell responses, and for
CC treating autoimmune disorders, hypersensitivity (e.g. allergic reaction),
CC CD8 versus host disease, or graft rejection. The present sequence is a
XX
SQ Sequence 235 AA;
Query Match 99.2%; Score 637; DB 6; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.1e-62;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SQRVSPDLRTWNLGETVELKQVLLSNPTSGCSWLPQPRGAASPTFLYLTSQNKPKA 61
DB 22 SQRVSPDLRTWNLGETVELKQVLLSNPTSGCSWLPQPRGAASPTFLYLTSQNKPKA 81
QY 62 EGLDTRFSGKRLGDTFVLLTSDFRRENGGYFCALSNSIMYFSGHFVVPFLPAKPTTTP 121
DB 82 EGLDTRFSGKRLGDTFVLLTSDFRRENGGYFCALSNSIMYFSGHFVVPFLPAKPTTTP 141
RESULT 9
ADD25613
ID ADD25613 standard; protein; 235 AA.
XX
AC ADD25613;
XX
DT 15-JAN-2004 (first entry)
XX
DB Binding domain-immunoglobulin fusion protein-associated protein #84.
XX
XX Binding domain-immunoglobulin fusion protein; cytostatic;
KW antitumor; immunosuppressive; antidiabetic; antithyroid;
KW neuroprotective; hinge region; immunoglobulin heavy chain;
KW CH2 constant region; CH3 constant region; IgG1;
KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX
OS Unidentified.
XX
PN US2003118592-A1.
XX
PD 26-JUN-2003.

XX 25-JUL-2002; 2002US-00207655.
PF 17-JAN-2001; 2001US-0367358P.
XX
PR 17-JAN-2002; 2002US-00053530.
XX
PR 03-JUN-2002; 2002US-0385691P.
XX
PA (GENE-) GENE-CRAFT INC.
XX
PI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
XX WPI; 2003-801317/75.
DR
XX
PT New binding domain-immunoglobulin fusion protein, useful for treating a
PT subject having or suspected of having a malignant condition or a B-cell
PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX
PS Disclosure; SEQ ID NO 174; 157pp; English.
XX
CC The invention relates to a binding domain-immunoglobulin fusion protein
CC comprising a binding domain polypeptide that is fused to an
CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
CC CH2 constant region polypeptide that is fused to the hinge region
CC polypeptide, and an immunoglobulin heavy chain CH3 constant region
CC polypeptide that is fused to the CH2 constant region polypeptide. The
CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin
CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
CC region polypeptide, derived from (a) having 3 or more cysteine residues;
CC where the mutated human IgG1 immunoglobulin hinge region polypeptide
CC contains 2 cysteine residues, where the first cysteine is not mutated; a
CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
CC (a) having 3 or more cysteine residues, where the mutated human IgG1
CC immunoglobulin hinge region polypeptide contains no more than one
CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
CC polypeptide, derived from (a) having 3 or more cysteine residues; where
CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains
CC no cysteine residues. The binding domain-immunoglobulin fusion protein is
CC capable of at least one immunological activity comprising antibody
CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
CC binding domain polypeptide is capable of specifically binding to an
CC antigen. Also included are an isolated polynucleotide encoding the
CC binding domain-immunoglobulin fusion protein, a recombinant expression
CC construct comprising the polynucleotide (operably linked to a promoter),
CC a host cell transformed or transfected with a recombinant expression
CC construct, producing the binding domain-immunoglobulin fusion protein, a
CC pharmaceutical composition comprising the binding domain-immunoglobulin
CC fusion protein or polynucleotide and a carrier, and treating a subject
CC having or suspected of having a malignant condition or a B-cell disorder.
CC The binding domain-immunoglobulin fusion protein is useful for treating a
CC subject having or suspected of having a malignant condition or a B-cell
CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
CC sclerosis or autoimmune disease. The present sequence is a binding domain
CC immunoglobulin fusion protein-associated protein sequence. Note: The
CC sequence data for this patent formed part of the printed specification
CC and is also available in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not
CC identified the sequences in the printed specification by their SEQ ID
CC number therefore none of the sequences can be explicitly identified.
XX
SQ Sequence 235 AA;
Query Match 99.2%; Score 637; DB 7; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.1e-62;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SQRVSPDLRTWNLGETVELKQVLLSNPTSGCSWLPQPRGAASPTFLYLTSQNKPKA 61
DB 22 SQRVSPDLRTWNLGETVELKQVLLSNPTSGCSWLPQPRGAASPTFLYLTSQNKPKA 81
QY 62 EGLDTRFSGKRLGDTFVLLTSDFRRENGGYFCALSNSIMYFSGHFVVPFLPAKPTTTP 121
DB 82 EGLDTRFSGKRLGDTFVLLTSDFRRENGGYFCALSNSIMYFSGHFVVPFLPAKPTTTP 141

```

RESULT 10
ADP12470
ID ADP12470 standard; protein; 235 AA.
XX
XX
AC ADP12470;
XX
XX
DT 12-AUG-2004 (first entry)
XX
XX
DE Protein encoded by mRNA of the invention #80.
XX
XX
KM transplant rejection; immune system; rheumatoid arthritis; lupus;
inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
XX
XX
OS Homo sapiens.
XX
XX
PN WO2004042346-A2.
XX
XX
PD 21-MAY-2004.
XX
XX
PF 24-APR-2003; 2003WO-US012946.
XX
XX
PR 24-APR-2002; 2002US-00131831.
XX
XX
PR 20-DEC-2002; 2002US-00325899.
XX
XX
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
XX
PI Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
Rosenberg S;
XX
XX
XX WPI; 2004-400724/37.
XX
XX
PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
rejection, in an individual, comprises detecting the expression level of
the genes.
XX
XX
PS Claim 65; SEQ ID NO 2479; 1762pp; English.
XX
XX
CC The present invention relates to diagnosing or monitoring transplant
rejection, e.g. cardiac or kidney transplant rejection, in an individual
comprises detecting the expression level of one or more genes. The
method, system and kits are useful in diagnosing or monitoring
transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
islet, lung, bone marrow or stem cell transplant rejection,
xenotransplant rejection or mechanical organ replacement rejection, in
an individual. The method is also useful in assessing the immune status of
an individual. The methods are also useful in diagnosing and monitoring
diseases that involve the immune system, e.g. rheumatoid arthritis,
lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
viral, bacterial or fungal infection. The present sequence represents a
protein that is encoded by the mRNA of the invention.
XX
XX
SQ Sequence 235 AA;
XX
XX
Query Match 99.2%; Score 637; DB 8; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.1e-62;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 2 SQFRVSPIDRTWNIGETVELKCVLLSNPTSGCSWLQPRGAASPTFLIYLSQNKPKAA 61
DB 22 SQFRVSPIDRTWNIGETVELKCVLLSNPTSGCSWLQPRGAASPTFLIYLSQNKPKAA 81
XX
QY 62 EGLDQRFSGKRLGDTFVLTLSDFRRENGGYFCALSINSIMYFSHFVVFPLPAKPTTP 121
DB 82 EGLDQRFSGKRLGDTFVLTLSDFRRENGGYFCALSINSIMYFSHFVVFPLPAKPTTP 141
XX
RESULT 11
ADQ18425
ID ADQ18425 standard; protein; 235 AA.
XX

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AC ADQ18425;
XX
XX
DT 26-AUG-2004 (first entry)
XX
XX
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1244.
XX
XX
KM soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
XX
XX
OS Homo sapiens.
XX
XX
PN WO2004048938-A2.
XX
XX
PD 10-JUN-2004.
XX
XX
PF 26-NOV-2003; 2003WO-US038193.
XX
XX
PR 26-NOV-2002; 2002US-0429739P.
XX
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
XX
PI Aziz N, Ginsburg WM, Zlotnick A;
XX
XX
XX WPI; 2004-441208/41.
XX
XX
DR Early detection of soft tissue sarcoma comprises determining expression
of a gene in a first soft tissue sample and a normal soft tissue sample
and comparing the gene expression, also useful in creating soft tissue
sarcoma.
XX
XX
PS Example 2; SEQ ID NO 1244; 210pp; English.
XX
XX
CC The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC protein of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX
XX
SQ Sequence 235 AA;
XX
XX
Query Match 99.2%; Score 637; DB 8; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.1e-62;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 2 SQFRVSPIDRTWNIGETVELKCVLLSNPTSGCSWLQPRGAASPTFLIYLSQNKPKAA 61
DB 22 SQFRVSPIDRTWNIGETVELKCVLLSNPTSGCSWLQPRGAASPTFLIYLSQNKPKAA 81
XX
QY 62 EGLDQRFSGKRLGDTFVLTLSDFRRENGGYFCALSINSIMYFSHFVVFPLPAKPTTP 121
DB 82 EGLDQRFSGKRLGDTFVLTLSDFRRENGGYFCALSINSIMYFSHFVVFPLPAKPTTP 141
XX
RESULT 12
ADB92816
ID ADB92816 standard; protein; 235 AA.
XX
XX
AC ADB92816;
XX
XX
DT 16-DEC-2004 (first entry)
XX
XX
DE Amino acid sequence of a CD8 alpha-chain protein.
XX
XX
KM immune response; cell-specific antigen; alloantigen; CD8;
CD8 alpha-chain; cellular immune response; humoral immune response;
transplant allograft; graft-versus-host disease; transplant.
XX

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XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..21
XX FT /note="signal peptide"
XX FT 183..210
XX FT Domain
XX FT /note = transmembrane domain
XX
XX MO2004083244-A2.
XX
XX PD 30-SEP-2004.
XX
XX PF 19-MAR-2004; 2004WO-US008574.
XX
XX PR 19-MAR-2003; 2003US-0456378P.
XX
XX PA (ISOG-) ISOGENTIS INC.
XX
XX PI Qi Y, Zhang X, Konigsberg PJ;
XX
XX DR WPI; 2004-691022/67.
XX
XX DR N-PSDB; ADS92817.
XX
XX PT Specifically inhibiting host immune responses to alloantigens, useful for
XX PT e.g. treating graft-versus-host disease, comprises contacting a target
XX PT cell expressing the antigen with an expression vector encoding a CD8
XX PT polypeptide.
XX
XX PS Disclosure; Fig 1; 98pp; English.
XX
XX CC The specification describes a method for specifically inhibiting a host
XX CC immune response to target cell-specific antigens (e.g. alloantigens). The
XX CC method comprises contacting a target cell expressing the antigen with an
XX CC expression vector encoding a CD8 polypeptide comprising the CD8 alpha-
XX CC chain, where the CD8 polypeptide is expressed by the target cell and
XX CC where the host immune response against the target cell is specifically
XX CC inhibited. The method of the invention is useful for specifically
XX CC inhibiting both cellular and humoral immune responses to alloantigens,
XX CC thus finding use in extending the survival of transplant allografts and
XX CC in treating graft-versus-host disease in transplant recipients. The
XX CC present sequence encodes the alpha-chain of a CD8 protein. This CD8 alpha
XX CC -chain may be used in the method of the invention.
XX
XX SQ Sequence 235 AA;
XX
XX Query Match 99.2%; Score 637; DB 8; Length 235;
XX Best Local Similarity 100.0%; Pred. No. 1.1e-62;
XX Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 SQFRVSPIDRTWNIGETVELKQVILSNPTSGCSWLFOPRGAASPTFLYLISQNKPKAA 61
XX DB 22 SQFRVSPIDRTWNIGETVELKQVILSNPTSGCSWLFOPRGAASPTFLYLISQNKPKAA 81
XX
XX QY 62 EGLDTRQFSGRKLGDTFVLTLSDFRRENGYFFCSALNSINIMYFSHFVVPFLPAKPTTP 121
XX DB 82 EGLDTRQFSGRKLGDTFVLTLSDFRRENGYFFCSALNSINIMYFSHFVVPFLPAKPTTP 141
XX
XX RESULT 13
XX ADS92790
XX ID ADS92790 standard; protein; 235 AA.
XX
XX AC ADS92790;
XX
XX DT 16-DEC-2004 (first entry)
XX
XX XX Amino acid sequence of a CD8 alpha-chain protein.
XX
XX KW immune response; cell-specific antigen; alloantigen; CD8;
XX KW CD8 alpha-chain; cellular immune response; humoral immune response;
XX KW transplant allograft; graft-versus-host disease; transplant.
XX

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OS OS Homo sapiens.
XX
XX PN MO2004083244-A2.
XX
XX PD 30-SEP-2004.
XX
XX PF 19-MAR-2004; 2004WO-US008574.
XX
XX PR 19-MAR-2003; 2003US-0456378P.
XX
XX PA (ISOG-) ISOGENTIS INC.
XX
XX PI Qi Y, Zhang X, Konigsberg PJ;
XX
XX DR WPI; 2004-691022/67.
XX
XX DR N-PSDB; ADS92791.
XX
XX PT Specifically inhibiting host immune responses to alloantigens, useful for
XX PT e.g. treating graft-versus-host disease, comprises contacting a target
XX PT cell expressing the antigen with an expression vector encoding a CD8
XX PT polypeptide.
XX
XX PS Disclosure; Fig 1; 98pp; English.
XX
XX CC The specification describes a method for specifically inhibiting a host
XX CC immune response to target cell-specific antigens (e.g. alloantigens). The
XX CC method comprises contacting a target cell expressing the antigen with an
XX CC expression vector encoding a CD8 polypeptide comprising the CD8 alpha-
XX CC chain, where the CD8 polypeptide is expressed by the target cell and
XX CC where the host immune response against the target cell is specifically
XX CC inhibited. The method of the invention is useful for specifically
XX CC inhibiting both cellular and humoral immune responses to alloantigens,
XX CC thus finding use in extending the survival of transplant allografts and
XX CC in treating graft-versus-host disease in transplant recipients. The
XX CC present sequence represents the alpha-chain of a CD8 protein. This CD8
XX CC alpha-chain may be used in the method of the invention.
XX
XX SQ Sequence 235 AA;
XX
XX Query Match 99.2%; Score 637; DB 8; Length 235;
XX Best Local Similarity 100.0%; Pred. No. 1.1e-62;
XX Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 SQFRVSPIDRTWNIGETVELKQVILSNPTSGCSWLFOPRGAASPTFLYLISQNKPKAA 61
XX DB 22 SQFRVSPIDRTWNIGETVELKQVILSNPTSGCSWLFOPRGAASPTFLYLISQNKPKAA 81
XX
XX QY 62 EGLDTRQFSGRKLGDTFVLTLSDFRRENGYFFCSALNSINIMYFSHFVVPFLPAKPTTP 121
XX DB 82 EGLDTRQFSGRKLGDTFVLTLSDFRRENGYFFCSALNSINIMYFSHFVVPFLPAKPTTP 141
XX
XX RESULT 14
XX ADS19436
XX ID ADS19436 standard; protein; 235 AA.
XX
XX AC ADS19436;
XX
XX DT 16-DEC-2004 (first entry)
XX
XX XX Human CD8 alpha chain protein.
XX
XX KW gene therapy; CD8 alpha chain; cellular immune response;
XX KW humoral immune response; immunosuppressive.
XX
XX OS Homo sapiens.
XX
XX PN MO2004083404-A2.
XX
XX PD 30-SEP-2004.
XX
XX PF 19-MAR-2004; 2004WO-US008567.
XX

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PT	19-MAR-2003; 2003US-0456378P.
XX	
XX	PA (ISOG-) ISOGENIS INC.
XX	
PI	Qi Y, Zhang X, Konigsberg PJ;
XX	
DR	WPI: 2004-691049/67.
XX	
DR	N-PSDB; ADS19437, ADS19462.
XX	
PT	New polynucleotide comprising a nucleic acid encoding a CD8 alpha-chain
PT	operably linked to a nucleic acid encoding a transmembrane polypeptide,
PT	useful for inhibiting cellular and humoral components of the host immune
PT	responses.
XX	
XX	
PS	Disclosure; Fig 1; 94pp; English.
XX	
CC	This invention relates to novel gene therapy vectors with reduced
CC	immunogenicity. Specifically, it refers to a nucleic acid encoding a CD8
CC	alpha chain operably linked to nucleic acid encoding a transmembrane
CC	polypeptide and a second nucleic acid representing the therapeutic gene
CC	of interest (for example oncolytic carboxyl transferase or beta
CC	glucosidase), whereby transcriptional and translational control elements
CC	direct expression thereof. The present invention describes a method to
CC	reduce an immune response against antigens derived from a gene therapy
CC	delivery system i.e. improving the expression of a therapeutic
CC	in a host and improving viral expression vectors with reduced
CC	immunogenicity. Accordingly, these compositions are useful for inhibiting
CC	both the cellular and humoral components of the host immune responses
CC	against expression vectors and target cells transfected with the vectors.
CC	As such, they exhibit immunosuppressive activity. This polypeptide is the
CC	human CD8 alpha chain protein of the invention.
XX	
XX	
Seq	Sequence 235 AA;
Query Match	99.2%; Score 637; DB 8; Length 235;
Best Local Similarity	100.0%; Pred. No. 1,1e-62;
Matches 120;	Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	2 SQFRVSPIDRTWNTGETVELKQVLLSNPTSGCSMWLPORGAAAPTFLLYISQKKPKXA 61
DB	22 SQFRVSPIDRTWNTGETVELKQVLLSNPTSGCSMWLPORGAAAPTFLLYISQKKPKXA 81
QY	62 EGLDQPSGSRIGTPTVLTISDFRRENGYFCSALNSITVPSHFVPLPAKPTTP 121
DB	82 EGLDQPSGSRIGTPTVLTISDFRRENGYFCSALNSITVPSHFVPLPAKPTTP 141
RESULT 15	
ADZ26402	
ID	ADZ26402 standard; protein; 235 AA.
XX	
XX	ADZ26402;
XX	
D7	16-JUN-2005 (first entry)
DE	
DE	Human CD8.
XX	
KM	cell culture; stem cell; CD8.
XX	
OS	Homo sapiens.
XX	
PN	MO2005030999-A1.
XX	
PD	07-APR-2005.
XX	
PF	24-SEP-2004; 2004WO-US031524.
XX	
PR	25-SEP-2003; 2003US-0506221P.
XX	
PR	08-OCT-2003; 2003US-0509594P.
XX	
PA	(DAND) DANA FABER CANCER INST INC.
XX	
PI	Ritz J, Wu CJ;
XX	

XX	WP1: 2005-273394/28.	
DR	N-PSDB; ADZ26401.	
XX		
PT	Detecting lineage-specific cells in a biological sample, useful for	
PT	determining the clinical outcome of a progenitor cell transfer in a	
PT	subject, comprises identifying lineage-specific mRNA in the sample.	
XX		
PS	Disclosure; SEQ ID NO 26; 393bp; English.	
XX		
CC	The invention relates to a method of detecting lineage-specific cells in	
CC	a biological sample which comprises identifying lineage-specific mRNA in	
CC	the sample. The methods are useful for determining the clinical outcome	
CC	of a progenitor cell transfer in a subject, and for identifying or	
CC	quantifying lineage-specific cells. The present sequence represents the	
CC	amino acid sequence of a human protein used to identify lineage-specific	
CC	cells.	
XX		
XX	Sequence 235 AA;	
XX		
Query Match	99.2%; Score 637; DB 9; Length 235;	
Best Local Similarity	100.0%; Pred. No. 1,1e-62;	
Matches 120; Conservative	0; Mismatches 0; Indels 0; Gaps 0	
Qy	2 SQFRVSPIDRTWNTGETVELKCOVLLSNPTSGCSWLFOPRGAASPTFLIYLSQNKPKAA 61	
Db	22 SQFRVSPIDRTWNTGETVELKCOVLLSNPTSGCSWLFOPRGAASPTFLIYLSQNKPKAA 81	
Qy	62 EGLDQNRSGKRLGDTFVLTLSDPRENEGYYFGSALNSINMYESHFVDFPAKPTTP 121	
Db	82 EGLDQNRSGKRLGDTFVLTLSDPRENEGYYFGSALNSINMYESHFVDFPAKPTTP 141	

Search completed: April 5, 2006, 15:54:11
Job time : 82 secs